

FIGURE 1

GGCTGAGGGGAGGCCCGGAGCCTTCTGGGGCCTGGGGGATCCTCTTGACATGGTGGGTGGA
GAGAAGCGCCTGCAGCCAACAGGGTCAGGCTGTGCTCACAGTTTCTCTGGCGGCATGTAA
AGGCTCCACAAAGGAGTTGGGAGTTCAAATGAGGCTGCTGCGGACGGCCTGAGGATGGACCC
CAAGCCCTGGACCTGCCGAGCGTGGCACTGAGGCAGCGGCTGACGCTACTGTGAGGGAAAGA
AGGTTGTGAGCAGCCCCGAGGACCCCTGGCCAGCCCTGGCCCCAGCCCTCTGCCGGAGCCCT
CTGTGGAGGCAGAGCCAGTGGAGCCCACTGAGGCAGGGCTGCTTGGCAGCCACCGGCCTGCA
ACTCAGGAACCCCTCCAGAGGCCATGGACAGGCTGCCCCGCTGACGGCCAGGGTGAAGCATG
TGAGGAGCCGCCCCGAGCCAAGCAGGAGGGAAGAGGCTTTCATAGATTCTATTACAAAGA
ATAACCACCATTTTGCAAGGACC**ATG**AGGCCACTGTGCGTGACATGCTGGTGGCTCGGACTG
CTGGCTGCCATGGGAGCTGTTGCAGGCCAGGAGGACGGTTTTTGAGGGCACTGAGGAGGGCTC
GCCAAGAGAGTTTCATTTACCTAAACAGGTACAAGCGGGCGGGCAGTCCCAGGACAAGTGCA
CCTACACCTTCATTTGCCCCAGCAGCGGGTCACGGGTGCCATCTGCGTCAACTCCAAGGAG
CCTGAGGTGCTTCTGGAGAACCAGTGCATAAGCAGGAGCTAGAGCTGCTCAACAAATGAGCT
GCTCAAGCAGAAGCGGCAGATCGAGACGCTGCAGCAGCTGGTGGAGGTGGACGGCGGCATTG
TGAGCCGAGGTGAAGCTGCTGCGCAAGGAGAGCCGCAACATGAACCTCGCGGGTCACGCAGCTC
TACATGCAGCTCCTGCACGAGATCATCCGCAAGCGGGACAACGCGTTGGAGCTCTCCAGCT
GGAGAACAGGATCCTGAACCAGACAGCCGACATGCTGCAGCTGGCCAGCAAGTACAAGGACC
TGGAGCACAAGTACCAGCACCTGGCCACACTGGCCCAACAACCAATCAGAGATCATCGCGCAG
CTTGAGGAGCACTGCCAGAGGGTGCCCTCGGCCAGGCCCGTCCCCAGCCACCCCCCGCTGC
CCCGCCCCGGGTCTACCAACCACCCACCTACAACCGCATCATCAACCAGATCTCTACCAACG
AGATCCAGAGTGACCAGAACCTGAAGGTGCTGCCACCCCTCTGCCCACTATGCCCACTCTC
ACCAGCCTCCCATCTTCCACCGACAAGCCGTGCGGCCCATGGAGAGACTGCCTGCAGGCCCT
GGAGGATGGCCACGACACCAGCTCCATCTACCTGGTGAAGCCGGAGAACACCAACCGCCTCA
TGCAGGTGTGGTGCGACCAAGACACGACCCCGGGGCTGGACCGTCATCCAGAGACGCTG
GATGGCTCTGTAACTTCTTACAGGAAGTGGGAGACGTACAAGCAAGGGTTTGGGAACATTGA
CGGCGAATACTGGCTGGGCCTGGAGAACATTTACTGGCTGACGAACCAAGGCAACTACAAAC
TCCTGGTGACCATGGAGGACTGGTCCGGCCGCAAAGTCTTTGAGAATACGCCAGTTTCCGC
CTGGAACCTGAGAGCGAGTATTATAAGCTGCGGCTGGGGCGCTACCATGGCAATGCGGGTGA
CTCCTTTACATGGCACAACGGCAAGCAGTTCACCACCCTGGACAGAGATCATGATGTCTACA
CAGGAAACTGTGCCCACTACCAGAAGGGAGGCTGGTGGTATAACGCCTGTGCCCACTCCAAC
CTCAACGGGGTCTGGTACCGCGGGGGCCATTACCGGAGCCGCTACCAGGACGGAGTCTACTG
GGCTGAGTTCCGAGGAGGCTCTTACTACTCAAGAAAGTGGTGATGATGATCCGACCGAACC
CCAACACCTTCCAC**TAA**GCCAGCTCCCCCTCTGACCTCTCGTGGCCATTGCCAGGAGCCCA
CCCTGGTCAGCTGGCCACAGCACAAAGAACAACCTCTCACCAAGTTCACTCTGAGGCTGGGA
GGACCGGGATGCTGGATTCTGTTTTCCGAAGTCACTGCAGCGGATGATGGAAGTGAATCGAT
ACGGTGTCTTCTGTCCCTCCTACTTTCTTTCACACAGACAGCCCCCTCATGTCTCCAGGACA
GGACAGGACTACAGACAACCTTTTCTTAAATAAATAAGTCTCTACAATAAAAAAA

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FIGURE 2

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA22779
><subunit 1 of 1, 493 aa, 1 stop
><MW: 57104, pI: 7.67, NX(S/T): 2
MRPLCVTCWWLGLLAAMGAVAGQEDGFEGTEEGSPREFIYLNRYKRAGESQDKCTYTFIVPQ
QRTGAICVNSKEPEVILENRVHKQELELLNNELLKQKRQIETLQQIVEVDGGIVSEVKLLR
KESRNMNSRVLTOLYMQLLHEIIRKRDNALELSQLENRILNQADMLQLASKYKDLEHKYQHL
ATLAHNQSEIIAQLEEHCQRPVPSARVPVQPPPAAPRVYQPPTYNRIINQISTNEIQSDQNL
KVLPPPLPTMPTLTSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTNRLMQVWCDQR
HDPGGWTVIQRRLDGSVNFFRNWETKQGFGNIDGEYWLGLENIYWLTNQGNKLLVTMEDW
SGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLDRDHDVYTGNCAYHQ
KGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKKVMMIRPNPNTFH
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Important features of the protein:**Signal peptide:**

amino acids 1-22

N-glycosylation sites.

amino acids 164-168, 192-196

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 124-128

Tyrosine kinase phosphorylation sites.

amino acids 177-184, 385-393, 385-394, 461-468

N-myristoylation sites.amino acids 12-18, 18-24, 22-28, 29-35, 114-120, 341-347,
465-471, 473-479**Amidation site.**

amino acids 373-377

Fibrinogen beta and gamma chains C-terminal domain signature.

amino acids 438-451

Fibrinogen beta and gamma chains C-terminal domain proteins.

amino acids 305-343, 365-402, 411-424, 428-458

Trehalase proteins.

amino acids 275-292

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FIGURE 3

CCCACGCGTCCGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACAAA
GGAGTCGCGCCGCCGCCGCCGCCCTCCCTCCGGTGGGCCCCGGGAGGTAGAGAAAGTCAGT
GCCACAGCCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCTGAGGGT
TGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACCGGACTGGG
GCCGGGTAGGCTCTGGAAAGGGCCCCGGGAGAGAGGTGGCGTTGGTCAGAACCTGAGAAACA
GCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTCCCTAGAAGAGGGT
GTTCCCTCTTTGGGGGTCCTCACCAGAAGAGGTTCTTGGGGGTCGCCCTTCTGAGGAGGCT
GCGGCTAACAGGGCCCAGAAGTGCATTGGATGTCCAGAATCCCCGTAGTTGATAATGTTG
GGAATAAGCTCTGCAACTTTCTTTGGCATTCACTTGTAAAAACAAATAGGATGCAAATTC
TCAACTCCAGGTTATGAAAACAGTACTTGAAAACTGAAAACTACCTAAATGATCGTCTTTG
GTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGGTCTGTTGTTGACTCTCGAAGAG
CACATAGCCCACTTCCTAGGGACTGGAGGTGCCGCTACTACCATGGGTAATTCCTGTATCTG
CCGAGATGACAGTGGAACAGATGACAGTGTTGACACCCAACAGCAACAGGCCGAGAACAGTG
CAGTACCCACTGCTGACACAAGGAGCCAACCACGGGACCCTGTTGCGCCACCAAGGAGGGGC
CGAGGACCTCATGAGCCAAGGAGAAAGAAACAAAATGTGGATGGGCTAGTGTTGGACACACT
GGCAGTAATACGGA CTCTGTAGATAAGTAAAGTATCTGACTCACGGTCACCTCCAGTGGAAT
GAAAAGTGTTCTGCCCGGAACCATGACTTTAGGACTCCTTCAGTTCCTTTAGGACATACTCG
CCAAGCCTTGCTGCTCACAGGGCAAAGGAGAATATTTTAATGCTCCGCTGATGGCAGAGTAAA
TGATAAGATTGATGTTTTTGCTTGCTGTCATCTACTTTGTCTGGAAATGTCTAAATGTTTC
TG TAGCAGAAAACACGATAAAGCTATGATCTTTATTAGAG

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FIGURE 5

CCCACGCGTCCGCGCAGTCGCGCAGTTCTGCCTCCGCCTGCCAGTCTCGCCCCGGATCCCCG
CCCCGGGCTGTGGCGTCGACTCCGACCCAGGCAGCCAGCAGCCCCGCGCGGGAGCCGGACCGC
CGCCGGAGGAGCTCGGACGGCATGCTGAGCCCCCTCCTTTGCTGAAGCCCAGTGC GGAGAA
GCCCCGGCAAACGCAGGCTAAGGAGACCAAAGCGGCGAAGTCGCGAGACAGCGGACAAGCAG
CGGAGGAGAAGGAGGAGGAGGCGAAGCCAGAGAGGGGCAGCAAAAGAAGCGGTGGTGGTGGG
CGTCGTGGCCATGGCGGCGGCTATCGCCAGCTCGCTCATCCGTCAGAAGAGGCAAGCCCCGCG
AGCGCGAGAAATCCAACGCCTGCAAGTGTGTACAGAGCCCCAGCAAAGGCAAGACCAGCTGC
GACAAAAACAAGTTAAATGTCTTTTCCGGGTCAAACCTCTTCGGCTCCAAGAAGAGGCGCAG
AAGAAGACCAGAGCCTCAGCTTAAGGGTATAGTTACCAAGCTATACAGCCGACAAGGCTACC
ACTTGCAGCTGCAGGCGGATGGAACCATGATGGCACCAAAGATGAGGACAGCACTTACACT
CTGTTTAACTCATCCCTGTGGGTCTGCGAGTGGTGGCTATCCAAGGAGTTCAAACCAAGCT
GTACTTGGCAATGAACAGTGAGGGATACTTGTACACCTCGGAACTTTTACACCTGAGTGCA
AATTCAAAGAATCAGTGTTTGAAAATTATTATGTGACATATTATCAATGATATACCGTCAG
CAGCAGTCAGGCCGAGGGTGGTATCTGGGTCTGAACAAAGAAGGAGAGATCATGAAAGGCAA
CCATGTGAAGAAGAACAAGCCTGCAGCTCATTTTCTGCCTAAACCACTGAAAGTGGCCATGT
ACAAGGAGCCATCACTGCACGATCTCACGGAGTTCTCCCGATCTGGAAGCGGGACCCCAACC
AAGAGCAGAAGTGTCTCTGGCGTGCTGAACGGAGGCAAATCCATGAGCCACAATGAATCAAC
GTAGCCAGTGAGGGCAAAGAAGGGCTCTGTAACAGAACCTTACCTCCAGGTGCTGTTGAAT
TCTTCTAGCAGTCCTTCACCCAAAAGTTCAAATTTGTGAGTGACATTTACCAAACAAACAGG
CAGAGTTCACTATTCTATCTGCCATTAGACCTTCTTATCATCCATACTAAAGC

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FIGURE 6

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA28498

><subunit 1 of 1, 245 aa, 1 stop

><MW: 27564, pI: 10.18, NX(S/T): 1

MAAAIASSLIRQKRQAREREKSNACKCVSSPSKGTSCDKNKLNVSFVKLFSGSKRRRRRP
EPQLKGIVTKLYSRQGYHLQLQADGTIDGTKDEDSTYTLFNLI PVGLRVVAIQGVQTKLYLA
MNSEGILYTSELF TPECKFKESVFENYYVTYSSMIYRQQQSGRGWYLG LNKEGEIMKGNHVK
KNKPAAHFLPKPLKVAMYKEPSLHDLTEFSRSGSGTPTKRSVSGVLNGGKSMHNEST

N-glycosylation site.

amino acids 242-246

Glycosaminoglycan attachment site.

amino acids 165-169, 218-222

Tyrosine kinase phosphorylation site.

amino acids 93-100

N-myristoylation site.

amino acids 87-93, 231-237

ATP/GTP-binding site motif A (P-loop).

amino acids 231-239

HBGF/FGF family proteins

amino acids 78-94, 102-153

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FIGURE 7

ATGGCCGCGGCCATCGCTAGCGGCTTGATCCGCCAGAAGCGGCAGGCGCGGGAGCAGCACTG
GGACCGGCCGCTCTGCCAGCAGGAGGCGGAGCAGCCCCAGCAAGAACCGCGGGCTCTGCAACG
GCAACCTGGTGGATATCTTCTCCAAAGTGCGCATCTTCGGCCTCAAGAAGCGCAGGTTGCGG
CGCCAAGATCCCCAGCTCAAGGGTATAGTGACCAGGTTATATTGCAGGCAAGGCTACTACTT
GCAAAATGCACCCCGATGGAGCTCTCGATGGAACCAAGGATGACAGCACTAATTCTACACTCT
TCAACCTCATACCAGTGGGACTACGTGTTGTTGCCATCCAGGGAGTGAAAACAGGGTTGTAT
ATAGCCATGAATGGAGAAGGTTACCTCTACCCATCAGAACTTTTTACCCCTGAATGCAAGTT
TAAAGAATCTGTTTTTGAAAATTATTATGTAATCTACTCATCCATGTTGTACAGACAACAGG
AATCTGGTAGAGCCTGGTTTTTTGGGATTAAATAAGGAAGGGCAAGCTATGAAAGGGAACAGA
GTAAAGAAAACCAAACCAGCAGCTCATTTTCTACCCAAGCCATTGGAAGTTGCCATGTACCG
AGAACCATCTTTGCATGATGTTGGGGAAACGGTCCCGAAGCCTGGGGTGACGCCAAGTAAAA
GCACAAGTGCGTCTGCAATAATGAATGGAGGCAAACCAGTCAACAAGAGTAAGACAACAT**TAG**

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FIGURE 8

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA28503

><subunit 1 of 1, 247 aa, 1 stop

><MW: 27702, pI: 10.36, NX(S/T): 2

MAAAIASGLIRQKRQAREQHWD RPSASRRRSSPSKNRGLCNGNLVDIFSKVRIFGLKKRRLR
RQDPQLKGIVTRLYCRQGYLQMHDPD GALTGTDSTNSTLFLNLI PVGLRVVAIQGVKTGLY
IAMNGEGYLYPSELF TPECKFKESVFENYYVIYSSMLYRQQESGRAWFLGLNKEGQAMKGNR
VKKTKPAAHFLPKPLEVAMYREPSLHDVGETVPKPGVTPSKSTSASAIMNGGKPVNKS KTT

N-glycosylation site.

amino acids 100-104, 242-246

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 28-32, 29-33

Tyrosine kinase phosphorylation site.

amino acids 199-207

N-myristoylation site.

amino acids 38-44, 89-95, 118-124, 122-128, 222-228

HBGF/FGF family proteins.

amino acids 104-155, 171-198

FIGURE 9

CTCGCAGCCGAGCGCGGCCGGGAAGGGCTCTCCTTCCAGCGCCGAGCACTGGGCCCTGGCA
GACGCCCCAAGATTGTTGTGAGGAGTCTAGCCAGTTGGTGAGCGCTGTAATCTGAACCAGCT
GTGTCCAGACTGAGGCCCATTTGCATTGTTTAACTACTTAGAAAATGAAGTGTTCATTTT
TAACATTCTCTCCAATTGGTTTAAATGCTGAATTACTGAAGAGGGCTAAGCAAAACCAGGT
GCTTGCAGCTGAGGGCTCTGCAGTGGCTGGGAGGACCCGGCCGTCTCCCCGTGTCTCTCCA
CGACTCGCTCGGCCCTCTGGAATAAAACACCCGCGAGCCCCGAGGGCCCAGAGGAGGCCGA
CGTGCCCGAGCTCTCCGGGGGTCCCGCCCGGAGCTTTCTTCTCGCCTTCGCATCTCTCTCC
TCGCGCGTCTTTGGACATGCCAGGAATAAAAAGGATACACTGTTACCATTCTGGCTCTCTG
TCTTCCAAGCCCTGGGAATGCACAGGCACAGTGCACGAATGGCTTTGACCTGGATCGCCAGT
CAGGACAGTGTTTAGATATTGATGAATGCCGAACCATCCCCGAGGCCTGCCGAGGAGACATG
ATGTGTGTTAACCAAAATGGCGGGTATTTATGCATTCGCCGGAACCCCTGTGTATCGAGG
GCCCCACTCGAACCCCTACTCGACCCCTACTCAGGTCCGTACCCAGCAGCTGCCCCACCAC
TCTCAGCTCCAACTATCCACGATCTCCAGGCCCTTATATGCCGCTTTGGATACCAGATG
GATGAAAGCAACCAATGTGTGGATGTGGACGAGTGTGCAACAGATTCCCACCAGTGAACCC
CACCCAGATCTGCATCAATACTGAAGCGGGGTACACCTGCTCCTGCACCCGAGGATATTGGC
TTCTGGAAGGCCAGTGTCTAGACATTGATGAATGTGCTATGGTACTGCCAGCAGCTCTGT
CGGAATGTTCTGGATCCTATTCTTGTACATGCAACCCCTGGTTTTACCCTCAATGAGGATGG
AAGGCTTTGCCAAGATGTGAACGAGTGTGCCACCGAGAACCCTGGCTGCAAACTGCGTCA
ACACCTACGGCTCTCTCATCTGCCGCTGTGACCCAGGATATGAATTGAGGAAGATGGCGTT
CATTGCAGTGATATGGACGAGTGCAGCTTCTCTGAGTTTCTCTGCCAACATGAGTGTGTGAA
CCAGCCCGGCACATACTTCTGCTCCTGCCCTCCAGGCTACATCCTGCTGGATGACAACCGAA
GCTGCCAAGACATCAACGAATGTGAGCACAGGAACACACGTGCAACCTGCAGCAGACGTGC
TACAATTTACAAGGGGGCTTCAAATGCATCGACCCCATCCGCTGTGAGGAGCCTTATCTGAG
GATCAGTGATAACCGTGTATGTGTCTGCTGAGAACCCCTGGCTGCAGAGACAGCCCTTTA
CCATCTGTACCGGGCATGGACGTGGTGTGAGGACGCTCCGTTCCCGCTGACATCTTCCAA
ATGCAAGCCACGACCCGCTACCCTGGGGCCTATTACATTTTCCAGATCAAATCTGGGAATGA
GGGCAGAGAATTTTACATGCGGCAACGGGCCCATCAGTGCCACCCTGGTGATGACACGCC
CCATCAAAGGGGCCCCGGGAAATCCAGCTGGACTTGGAAATGATCACTGTCAACACTGTCTC
AACTTCAGAGGCAGCTCCGTGATCCGACTGCGGATATATGTGTGCGAGTACCCATTCTGAGC
CTCGGGCTGGAGCCTCCGACGCTGCCCTCTATTGGCACCAAGGGACAGGAGAAGAGAGGAAA
TAACGAGAGAGAATGAGAGCGACACAGACGTTAGGCATTTCCCTGCTGAACGTTTTCCCGAAGA
GTCAGCCCCGACTTCTTGACTCTCACCTGTACTATTGCAGACCTGTCAACCTGCAGGACTTG
CCACCCCCAGTTCCATGACACAGTTATCAAAAAGTATTATCATTTGCTCCCCGTATAGAAGA
TTGTTGGTGAATTTTCAAGGCCTTCAGTTTATTTCCACTATTTTCAAAGAAAATAGATTAGG
TTTGCGGGGGTCTGAGTCTATGTTCAAAGACTGTGAACAGCTTGTGTCACTTCTTTCACCTC
TTCCACTCCTTCTCTCACTGTGTTACTGCTTTTGCAAAGACCCGGGAGCTGGCGGGGAACCC
GGGAGTAGCTAGTTTGCTTTTGGCGTACACAGAGAAGGCTATGTAACAAACACAGCAGGA
TCGAAGGGTTTTTAGAGAATGTGTTTCAAAACCATGCCGTGTTATTTCAACCATAAAAGAAG
TTTCAGTTGTCCTTAAATTTGTATAACGGTTTAAATCTGTCTTGTTTCATTTTGAGTATTTTT
AAAAAATATGTCGTAGAATTCTTCCGAAAGGCCTTCAGACACATGCTATGTTCTGTCTTCCC
AAACCCAGTCTCCTCTCCATTTTCCAGTGTGTTTCTGAGGACCCCTTAATCTGTCTTT
CTTTAGAAATTTTACCCTAATTGGATTGGAATGCAGAGGTCTCCAACTGATTAATATTTGA
AGAGA

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FIGURE 10

MPGIKRILTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQ
NGGYLCIPRTNPVYRGPYSNPYSTPYSGPYAAAAPPLSAPNYPTISRPLICRFGYQMDESNQ
CVDVDECATDSHQCNPTQICINTEGGYTCSDTDGYWLLEGQCLDIDECRYGYCQQLCANVPG
SYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSLICRCDPGYELEEDGVHCSDM
DECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQG
GFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFITILYRDMDVVSGRSVPADIFQMQATT
RYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDLEMITVNTVINFRGS
SVIRLRIYVSQYPF

Important features of the protein:**Signal peptide:**

amino acids 1-25

N-glycosylation sites.

amino acids 283-287, 296-300

N-myristoylation sites.amino acids 21-27, 64-70, 149-155, 186-192, 226-232, 242-248,
267-273, 310-316**Aspartic acid and asparagine hydroxylation sites.**

amino acids 144-156, 181-193, 262-274

Cell attachment sequence.

amino acids 54-57

Calcium-binding EGF-like.

amino acids 131-166, 172-205, 211-245, 251-286

FIGURE 11

CAGGTCCAACTGCACCTCGGTTCTATCGATTGAATTCCTCCCGGGGATCCTCTAGAGATCCCTC
GACCTCGACCCACGCGTCCGAACACAGGTCCTTGTGCTGCGAGAGAAGCAGTTGTTTTGCTG
GAAGGAGGGAGTGC GCGGGCTGCCCCGGGCTCCTCCTGCCGCCTCCTCTCAGTGGATGGTT
CCAGGCACCTGTCTGGGGCAGGGAGGGCACAGGCCTGCACATCGAAGGTGGGGTGGGACCA
GGTGCCCTCGCCCCAGCATCCAAGTCCTCCCTTGGGCGCCCTGGCCCTGCAGACTCTCA
GGGCTAAGGTCCTCTGTTGCTTTTTTGGTTCCACCTTAGAAGAGGCTCCGCTTGACTAAGAGT
AGCTTGAAGGAGGCACCA**ATG**CAGGAGCTGCATCTGCTCTGGTGGGCGCTTCTCCTGGGCGCTG
GCTCAGGCCTGCCCTGAGCCCTGCGACTGTGGGGAAGATATGGCTTCCAGATCGCCGACTG
TGCCTACCGCGACCTAGAATCCGTGCCGCTGGCTTCCCGGCCAATGTGACTACACTGAGCC
TGTCAGCCAACCGGCTGCCAGGCTTGCCGGAGGGTGCTTCAGGGAGGTGCCCTGCTGCAG
TCGCTGTGGCTGGCACACAATGAGATCCGCACGGTGGCCGCCGGAGCCCTGGCCTCTCTGAG
CCATCTCAAGAGCCTGGACCTCAGCCACAATCTCATCTGACTTTGGCTGGAGCGACCTGC
ACAACCTCAGTGCCCTCCAATTGCTCAAGATGGACAGCAACGAGCTGACCTTCATCCCCCGC
GACGCCTTCCGCAGCCTCCGTGCTCTGCGCTCGCTGCAACTCAACCACAACCGCTTGACAC
ATTGGCCGAGGGCACCTTACCCCGCTCACC GCGCTGTCCACCTGCAGATCAACGAGAACC
CCTTCGACTGCACCTGGGCGATCGTGTGGCTCAAGACATGGGCCCTGACCACGGCCGTGTCC
ATCCCCGAGCAGGACAACATCGCCTGCACCTCACCCTCATGTGCTCAAGGGTACCCGCTGAG
CCGCTGCCGCCACCTGCCATGCTCGGCGCCCTCAGTGCAGCTCAGCTACCAACCGCCAGG
ATGGTGCCGAGCTGCGGCTGTTTTGTGCTGGCACTGCACTGTGATGTGGACGGGCAGCCG
GCCCCCTCAGCTTCACTGGCACATCCAGATACCCAGTGGCATTGTGGAGATCAACGACCCCAA
CGTGGGCACTGATGGGCGTGCCCTGCCTGGCACCCCTGTGGCGAGTCCCAGCCGCGCTTCC
AGGCCTTTGCCAATGGCAGCCTGCTTATCCCCGACTTTGGCAAGCTGGAGGAAGGCACCTAC
AGCTGCCGTGGCCACCAATGAGCTGGGCACTGCTGAGAGCTCAGTGGACGTGGCACTGGCCAC
GCCCCGTGAGGGTGGTGAGACACACTGGGGCGCAGGTTCCATGGCAAAGCGGTTGAGGGAA
AGGGCTGCTATACGGTTGACAACGAGGTGCAGCCATCAGGGCCGGAGGACAATGTGGTCATC
ATCTACCTCAGCCGTGCTGGGAACCTGAGGCTGCAGTCGCAGAAGGGGTCCCTGGGCAGCT
GCCCCAGGCCTGCTCCTGCTGGGCCAAAGCCTCCTCCTTCTTCTTCTCCTCACCTCCTTCT
AGCCCCACCCAGGGCTTCCCTAACTCCTCCCTTGCCCTACCAATGCCCTTTAAGTGCTG
CAGGGGTCTGGGGTTGGCAACTCCTGAGGCCTGCATGGGTGACTTCACATTTTCTACCTCT
CCTTCTAATCTCTTCTAGAGCACCTGCTATCCCCAACTTCTAGACCTGCTCCAACCTAGTGA
CTAGGATAGAATTTGATCCCCCTAACTCACTGTCTGCGGTGCTCATGTCTGCTAACAGCATTG
CCTGTGCTCTCCTCTCAGGGGCAGCATGCTAACGGGGCGACGTCTTAATCCAAGTGGGAGAA
GCCTCAGTGGTGGAATTTCCAGGCACTGTGACTGTCAAGCTGGCAAGGGCCAGGATTGGGGGA
ATGAGAGTGGGGCTAGCTGGGAGGTGGTCTGAAGCAGACAGGGAATGGGAGAGGAGGATGG
GAAGTAGACAGTGGCTGGTATGGCTTGAGGCTCCTGGGCTGCTCAAGCTCCTCCTGCT
CCTTGTGTTTTCTGATGATTTGGGGGCTTGGGAGTCCCTTTGTCTCATCTGAGACTGAAA
TGTGGGGATCCAGGATGGCCTTCCTTCTTACCCTTCTCCTCCCTCAGCCTGCAACCTCTAT
CCTGGAACTGTCCTCCTCCTTTCTCCCAACTATGCATCTGTTGTGCTCCTCCTGCAAGGC
CAGCCAGCTTGGGAGCAGCAGAGAAATAAACAGCATTTCTGATGCCAAAAAAAAAAAAAAAA
AAGGGCGGCGCGACTCTAGAGTCGACCT

FIGURE 13

CCAGGCCGGGAGGCGACGCGCCAGCCGTCTAAACGGGAACAGCCCTGGCTGAGGGAGCTGC
AGCGCAGCAGAGTATCTGACGGCGCCAGGTTGCGTAGGTGCGGCACGAGGAGTTTCCCGGC
AGCGAGGAGGTCTGAGCAGCATGGCCCGGAGGAGCGCCTTCCCTGCCGCCGCGCTCTGGCT
CTGGAGCATCCTCCTGTGCCTGCTGGCACTGCGGGCGGAGGCCGGGCCGCGCAGGAGGAGA
GCCTGTACCTATGGATCGATGCTCACCAGGCAAGAGTACTCATAGGATTTGAAGAAGATATC
CTGATTGTTTTAGAGGGGAAAATGGCACCTTTTACACATGATTTAGAAAAGCGCAACAGAG
AATGCCAGCTATTCTGTCAATATCCATTCCATGAATTTTACCTGGCAAGCTGCAGGGCAGG
CAGAATACTTCTATGAATTCTGTCTTTCGCTCCCTGGATAAAGGCATCATGGCAGATCCA
ACCGTCAATGTCCCTCTGCTGGGAACAGTGCCCTACAAGGCATCAGTTGTTCAAGTTGGTTT
CCCATGCTTGGAAAACAGGATGGGGTGGCAGCATTTGAAGTGGATGTGATTGTTATGAATT
CTGAAGGCAACACCATTCTCCAAACACCTCAAATGCTATCTTCTTTAAAACATGTCAACAA
GCTGAGTGCCAGGCGGGTGCCGAAATGGAGGCTTTTGTAATGAAAGACGCATCTGCGAGTG
TCCTGATGGGTTCACGGACCTCACTGTGAGAAAGCCCTTTGTACCCACGATGTATGAATG
GTGGACTTTGTGTGACTCCTGTTTCTGCATCTGCCCACCTGGATTCTATGGAGTGAAGTGT
GACAAAGCAAACCTGCTCAACCACCTGCTTTAATGGAGGGACCTGTTTCTACCTTGAAAATG
TATTTGCCCTCCAGGACTAGAGGGAGAGCAGTGTGAAATCAGCAAATGCCACAACCCTGTC
GAAATGGAGGTAAATGCATTGGTAAAGCAAATGTAAGTGTTCAAAGGTTACCAGGGAGAC
CTCTGTTCAAAGCCTGTCTGCGAGCCTGGCTGTGGTGCACATGGAACCTGCCATGAACCCAA
CAAATGCCAATGTCAAGAAGGTTGGCATGGAAGACACTGCAATAAAAGGTACGAAGCCAGCC
TCATACATGCCCTGAGGCCAGCAGCGCCAGCTCAGGCAGCACACGCCTTCACTTAAAAAG
GCCGAGGAGCGGCGGGATCCACCTGAATCCAATTACATCTGGTGAACTCCGACATCTGAAAC
GTTTTAAGTTACACCAAGTTCATAGCCTTTGTTAACCTTTCATGTGTTGAATGTTCAAATAA
TGTTCAATTACACTTAAGAATACTGGCCTGAATTTTATTAGCTTCATTATAAATCACTGAGCT
GATATTTACTCTTCCTTTTAAGTTTTCTAAGTACGCTCTGTAGCATGATGGTATAGATTTTCT
TGTTTCAGTGCTTTGGGACAGATTTTATATTATGTCAATTGATCAGGTTAAAAATTTTCAGTG
TGTAGTTGGCAGATATTTTCAAATTTACAATGCATTTATGGTGTCTGGGGGCAGGGGAACAT
CAGAAAGGTTAAATTTGGGCAAAAATGCGTAAAGTCACAAGAATTTGGATGGTGCAGTTAATGT
TGAAGTTACAGCATTTTCAGATTTTATTGTGATATTTTAGATGTTTGTACATTTTAAAAA
TTGCTCTTAATTTTTTAACTCTCAATACAATATATTTTGACCTTACCATTATTCCAGAGATT
CAGTATTAATAAAAAAAAAAATTACACTGTGGTAGTGGCATTTAAACAATATAATATATTCTA
AACACAATGAAATAGGGAATATAATGTATGAACTTTTGCATTGGCTTGAAGCAATATAATA
TATTGTAAACAAAACACAGCTCTTACCTAATAAACATTTTATACTGTTTGTATGTATAAAAT
AAAGGTGCTGCTTTAGTTTTTTGGAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 14

MARRSAFPAAALWLWSILLCLLALRAEAGPPQEESSLYLWIDAHQARVLIGFEEDILIVSEGK
MAPFTHDFRKAQQRMPAIPVNIHSMNFTWQAAGQAIFYEFSLRSLDKGIMADPTVNVPLL
GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPPGGC
RNGGFCNERRICECPDGFHGHPCHEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCST
TCFNGGTCTFYPGKCICPPGLEGEQCEISKCPQPCRNGGKCIGKSKCKCSKGYQGDLCSKPVC
EPGCGAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAEEERDP
PESNYIW

Signal sequence.

amino acids 1-28

N-glycosylation sites.

amino acids 88-92, 245-249

Tyrosine kinase phosphorylation site.

amino acids 370-378

N-myristoylation sites.

amino acids 184-190, 185-191, 189-195, 315-321

ATP/GTP-binding site motif A (P-loop).

amino acids 285-293

EGF-like domain cysteine pattern signature.

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

16/75

FIGURE 16

MMGLSLASAVLLASLLSLHLGTATRGSDISKTCFQYSHKPLPWTWVRSYEFTSNCSQRAV
IFTTKRGKKVCTHPRKKWVQKYISLLKTPKQL

Important features of the protein:

Signal peptide:

amino acids 1-23

N-myristoylation sites.

amino acids 3-9, 26-32

Amidation site.

amino acids 68-72

Small cytokines (intecrine/chemokine).

amino acids 23-88

17/75

FIGURE 17

GCGAGAACCCTTGCACGCGCACAACTACGGGGACGATTCTGATTGATTTTGGCGCTTTCGATCCACCCTCC
 TCCTTCTCATGGGACTTTGGGGACAAAGCGTCCCGACCGCTCGAGCGCTCGAGCAGGGCGCTATCCAGGAGC
 CAGGACACGCTCGGGAACACGACCATGGCTCTCGACCCCAAGATCCTTAAGTTCGTCTTCATCGTCGCGG
 TTCTGCTGCCGGTCCGGGTGACTCTGCCACCATCCCCGGCAGGACGAAGTTCGCCAGCAGACGTGGCCCCA
 CAGCAACAGAGGCGCAGCTCAAGGAGGAGGAGTGTCCAGCAGGATCTCATAGATCAGAAATATACTGGAGCGCTG
 TAACCCGTGCACAGAGGGTGTGGATTACACATTGCTTCCAACAATTTGCCCTTGTGCTGCTATGTACAGTTT
 GTAATCAGGTCAAACAAATAAAGTTCTGTACCACGACAGACACCGTGTGTCAGTGTGAAAAAGGAAGC
 TTCCAGGATAAAAACTCCCTGAGATGTGCCGACGTGTAGAACAGGGTGTCCAGAGGGATGGTCAAGGTCA
 TAATTGTACGCCCGGAGTGACATCAAGTGCAAAATGAATCAGCTGCCAGTTTCACTGGGAAAAACCCAGCAG
 CGGAGGAGACAGTGACCACCATCCTGGGGATGCTTGCTCTCCCTATCACTACCTTATCATCATAGTGGTTTTA
 GTCATCATTTTAGCTGTGGTTGGTTGGCTTTTCATGTGCGGAAGAATTCATTCTTACCTCAAAGGCATCTG
 CTCAGGTGGTGGAGGAGGTCCCCAAGCTGTGCACAGAGTCCTTTCCGGCGCGCTTCATGTCTTCCAGAGTTC
 CTGGGGCGGAGGACAATGCCCGCAACGAGACCTGAGTAACAGATACTTGACGCCACCCAGGTCTCTGAGCAG
 GAAATCCAAGGTGAGGAGCTGGCAGAGCTAACAGGTGTGACTGTAGAGTGCACAGAGGAGCCACAGCGTCTGTG
 GGAACAGGCAGAAGCTGAAGGGTGTCAAGAGGAGGAGGCTGCTGTTCCAGTGAATGACCTGACTCCGCTGACA
 TCAGCAGCTTCTGTGATGCTCGGCAACACTGGAAGAAGGACATGCAAGGAAACAATTCAGGACCAACTGGTG
 GGCTCCGAAAAGCTCTTTATGAAGAAGATGAGGAGGCTCTGCTAGCTCCTGCCGTGGAAGAATCTCTTCAG
 GAAACAGAGCTTCCCTCATTTACCTTTCTCTACAAAGGGAAGCAGCCGTGGAAGAACAGTCCAGTACTTGA
 CCCATGCCCCAACAACTCTACTATCCAATATGGGGCAGCTTACCAATGGTCCCTAGAATTTGTTAACGCAGTT
 GGAGTAATTTTATGAAATACTGCGTGTGATAAGCAACGGGAGAAATTTATATCAGATTCTTGGCTGCATAGT
 TATACGATTGTGATTAAGGGTGGTTTAGGCCACATGCGGTGGCTCATGCTGTAAATCCAGCAGCTTTGATAG
 GCTGAGGCAGGTGGATTGCTTGACTCGGGAGTTTGAGACAGCCTCATCAACAGTGAATCTCATCTCAAT
 TTAAGGAGAAAAAGTGGTTTTAGGATGTCACTTTTGCGAGTTCCTCATCATGAGCAAGTCTTTTTTCTGCTG
 TTCTTATATTGCAAGCTCCATCTCTACTGGTGTGTGCATTTAATGACATCTAATACAGATGCCGCACAGCCAC
 AATGCTTTGCCCTTATAGTTTTTAACTTTAGAACGGGATTATCTTGTTATTACCTGTATTTTCAGTTTCGGATA
 TTTTGTACTTAAATGATGAGATTATCAAGACGTAGCCCTATGCTAAGTCATGAGCATATGGACTACGAGGGTTC
 GACTTAGAGTTTTGAGCTTTAAGATAGGATTATTGGGGCTTACCCCACTTAAATAGAGAAACATTATATTG
 CTTACTACTGTAGGCTGTACATCTCTTTCCGATTTTGTGATAATGATGTAACATGGAAAACTTTAGGAAAT
 GCACCTTATTAGCTGTTTACATGGGTTGCCGATACAATCAGCAGTCAAAATGACTAAAAATATACTAGT
 GACGGAGGGAGAAATCCTCCCTCTGTGGGAGGCATCTACTGCATCTCAGTTCTCCCTCTCGCGCCCTGAGACTG
 GACCAGGGTTTGATGGCTGGCAGCTTCTCAAGGGGCAGCTTGCTTACTTGTAAATTTAGAGGTATATAGCCA
 TATTTATTTATAAAATAAATATTTATTTATTTATTTATAAGTAGATGTTTACATATGCCAGGATTTTGAAGAGC
 CTGGTATCTTTGGGAAGCCATGTGCTGGTGTGTCGTGCTGGGACAGTCATGGGACTGCATCTCCGACTTGTC
 CACAGCAGATGAGGACAGTGAGAAATTAAGTTAGATCCGAGACTGCGAAGAGCTTCTCTTCAAGCGCATTAACA
 GTTGAACGTTAGTGAATCTTGAGCCTCATTTGGGCTCAGGGCAGAGCAGGTGTTATCTGCCCGGCATCTGCC
 ATGGCATCAAGAGGAAGAGTGACGGTGTCTGGGAATGGTGAATGGTTGCCGACTCAGGCATGGATGGGC
 CCCTCTCGCTCTGCTGGTCTGTGAACGTAGTCCCTGGGATGCTTTAGGGGCAGAGATTCCTGAGCTGCGTTT
 TAGGGTACAGATTCCCTGTTGAGGAGCTTGCCGCCCTCTGTAAGCATCTGACTCATCTCAGAGATATCAATCT
 TAAACACTGTGACAACGGGACTTAAATGGCTGACACATTTGTCCCTGTGTGTCAGTTCATATTTTATTTAA
 AACCTCAGTAATCGTTTTAGCTTCTTTCCAGCAAACTCTTCTCCAGATAGCCCACTGCTGGTAGGATAAATA
 CGGATATGTCATCTTAGGGTTTCACTTTTCCATCTCAAGGCATTTGTGTTTGTGTTGTTCCGGACTGGTTT
 GCTGGGCAAAAGTTAGAATGCTGTAAGTTCCGACATTGAGATTGTTGTGTCCATGGAGTTTATAGGAGGGATG
 GCCTTTCCGGTCTTCGCACTTCCATCTCTCCACTTCCATCTGGCGTCCCACTCTGTCCCTGCACTTCTG
 GATGACACAGGGTGTGCTGCTGCTGCTGCTGCTTGTGCTTGTGCTGGGCTTGTGCGAGGAGACTTGGTCTCAA
 CTCAGAGAGAGCCAGTCCGGTCCAGCTCCTTTGCTCCCTTCCCTCAGAGGCTTCTTGAAGATGCACTAGACT
 ACCAGCCTTATCAGCTTATAGCTTATCTTTAAACATAAGCTTCTGACAAACATGAATTTGTTGGGGTTTTT
 GCGGTTGGTGTATTTGTTAGGTTTTGCTTTATACCCGGGCCAAATAGCACATAACACCTGGTTATATATGAAA
 TACTCATATGTTTATGACCAAAATAAATATGAAACCTCATRTTAAAAAAAAAAAAAAAAAAAAAAAAAAAA

18/75

FIGURE 18

MGLWGQSVPTASSARAGRYPGARTASGTRPWLLDPKILKFVVFIVAVLLPVRVDSATIPRQD
EVPQQTVAPOQQRRSLKEEECPAGSHRSEYTGACNPCTEGVDYTIASNNLPSCLLCTVCKSG
QTNKSSCTTTRDTVCQCEKGSFQDKNSPEMCRTCRTGCPRGMVKVSNCTPRSDIKCKNESAA
SSTGKTPAAEETVTITILGMLASPHYLIIVVLVIIILAVVVVGFSCRKKFISYLGKICSGGG
GGPERVHRVLFRRRSCPSRVPGAEDNARNETLSNRYLQPTQVSEQEIQGQELAEITGVTVES
PEEPQRLLEQAAEAGCQRRRLLPVNDADSADISTLLDASATLEEGHAKETIQDQLVGSEKL
FYEEDEAGSATSCL

Important features of the protein:**Transmembrane domains:**

amino acids 35-52, 208-230

N-glycosylation sites.

amino acids 127-131, 182-186, 277-281

Glycosaminoglycan attachment site.

amino acids 245-249

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 260-264

N-myristoylation sites.amino acids 21-27, 86-92, 102-108, 161-167, 242-248, 270-276,
297-303, 380-386**ATP/GTP-binding site motif A (P-loop).**

amino acids 185-193

TNFR/NGFR cysteine-rich region.

amino acids 99-139

19/75

FIGURE 19

CGGGCACCTGGAAGATGCGCCCATTGGCTGGTGGCCTGCTCAAGGTGGTGTTCGTGGTCTTC
GCCTCCTTGTGTGCCTGGTATTCGGGGTACCTGCTCGCAGAGCTCATTCCAGATGCACCCCT
GTCCAGTGCTGCCTATAGCATCCGCAGCATCGGGGAGAGGCCTGTCCTCAAAGCTCCAGTCC
CCAAAAGGCAAAATGTGACCACTGGACTCCCTGCCCATCTGACACCTATGCCTACAGGTTA
CTCAGCGGAGGTGGCAGAAGCAAGTACGCCAAAATCTGCTTTGAGGATAACCTACTTATGGG
AGAACAGCTGGGAAATGTTGCCAGAGGAATAAACATTGCCATTGTCAACTATGTAACCTGGGA
ATGTGACAGCAACACGATGTTTTGATATGTATGAAGGCGATAACTCTGGACCGATGACAAAG
TTTATTCAGAGTGCTGCTCCAAAATCCCTGCTCTTCATGGTGACCTATGACGACGGAAGCAC
AAGACTGAATAACGATGCCAAGAATGCCATAGAAGCACTTGGAAGTAAAGAAATCAGGAACA
TGAAATTCAGGTCTAGCTGGGTATTTATTGCAGCAAAGGCTTGGAACCTCCCTCCGAAATT
CAGAGAGAAAAGATCAACCACTCTGATGCTAAGAACAACAGATATTCTGGCTGGCCTGCAGA
GATCCAGATAGAAGGCTGCATACCCAAAGAACGAAGCTTGACACTGCAGGGTCCTGAGTAAAT
GTGTTCTGTATAACAAATGCAGCTGGAATCGCTCAAGAATCTTATTTTTCTAAATCCAACA
GCCCATATTTGATGAGTATTTTGGGTTTGTTGTAAACCAATGAACATTTGCTAGTTGTATCA
AATCTTGGTACGCAGTATTTTTATACCAGTATTTTATGTAGTGAAGATGTCAATTAGCAGGA
AACTAAATGAATGGAAATTCTTAAAAAAAAA

20/75

FIGURE 20

MRPLAGLLKVVVFVVFASLCAWYSGYLLAELIPDAPLSSAAYSIRSIGERPVLKAPVPKRQK
CDHWTPCPSDTYAYRLLSGGGRSKYAKICFEDNLLMGEQLGNVARGINIAIVNYVTGNVTAT
RCFDMYEGDNSGPMTKFIQSAAPKSLLFMVTYDDGSTRLNNDAKNAIEALGSKEIRNMKFRS
SWVFIAAKGLELPSEIQREKINHSDAKNNRYSGWPAEIQIEGCIPKERS

Important features of the protein:

Signal peptide:

amino acids 1-20

N-glycosylation sites.

amino acids 120-124, 208-212

Glycosaminoglycan attachment site.

amino acids 80-84

N-myristoylation sites.

amino acids 81-87, 108-114, 119-125

21/75

FIGURE 21

CCGGGGAGGGGAGGGCCCCGTCCCGCCCCCTCCCCGTCTCTCCCCGCCCCCTCCCCGTCCCTCCC
GCCGAAGCTCCGTCCCGCCCCGCGGGCCGGCTCCGCCCTCACCTCCCGGCCGCGGCTGCCCTC
TGCCCGGGTTGTCCAAGATGGAGGGCGCTCCACCGGGGTCGCTCGCCCTCCGGCTCCTGCTG
TTCGTGGCGCTACCCGCCTCCGGCTGGCTGACGACGGGCGCCCCGAGCCGCCGCCGCTGTC
CGGAGCCCCACAGGACGGCATCAGAATTAATGTAACCTACACTGAAAGATGATGGGGACATAT
CTAAACAGCAGGTTGTTCTTAACATAACCTATGAGAGTGGACAGGTGTATGTAAATGACTTA
CCTGTAAATAGTGGTGTAACCCGAATAAGCTGTCAGACTTTGATAGTGAAGAATGAAAATCT
TGAAAATTTGGAGGAAAAAGAATATTTTGGAAATTGTCAGTGTAAGGATTTTAGTTCATGAGT
GGCCTATGACATCTGGTTCCAGTTTGCAACTAATTGTCATTCAAGAAGAGGTAGTAGAGATT
GATGGAAAACAAGTTCAGCAAAAGGATGTCAGTCAAATTGATATTTTAGTTAAGAACCGGGG
AGTACTCAGACATTCAAACCTATACCCCTCCCTTTGGAAGAAAGCATGCTCTACTCTATTTCTC
GAGACAGTGACATTTTATTTACCCTTCCTAACCTCTCCAAAAAAGAAAGTGTTAGTTCAGTG
CAAACCACTAGCCAGTATCTTATCAGGAATGTGGAAACCACTGTAGATGAAGATGTTTTACC
TGGCAAGTTACCTGAAACTCCTCTCAGAGCAGAGCCGCCATCTTCATATAAGGTAATGTGTC
AGTGGATGGAAAAGTTTAGAAAAGATCTGTGTAGGTTCTGGAGCAACGTTTTCCAGTATTC
TTTCAGTTTTTTGAACATCATGGTGGTTGGAATTACAGGAGCAGCTGTGGTAATAACCATCTT
AAAGGTGTTTTTCCAGTTTCTGAATACAAAGGAATCTTCAGTTGGATAAGTGGACGTCA
TACCTGTGACAGCTATCAACTTATATCCAGATGGTCCAGAGAAAAGAGCTGAAAACCTTGAA
GATAAAACATGTATTTAAACGCCATCTCATATCATGGACTCCGAAGTAGCCTGTTGCCTCC
AAATTTGCCACTTGAATATAATTTTCTTTAAATCGTT

22/75

FIGURE 22

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60783
><subunit 1 of 1, 330 aa, 1 stop
><MW: 36840, pI: 4.84, NX(S/T): 4
MEGAPPGSLALRLLLFVALPASGWLTTGAPEPPPLSGAPQDGIRINVTTLKDDGDISKQQVV
LNITYESGQVYVNDLPVNSGVTRISCQTLIVKNENLENLEEKEYFGIVSVRILVHEWPMTSG
SSLQLIVIQEEVVEIDGKQVQKDVTEIDILVKNRGVLRHSNYTLPLEESMLYSISRSDIL
FTLPNLSKKESVSSLQTTSQYLIRNVETTVDEDVLPGLPETPLRAEPPSSYKVMCQWMEKF
RKDLCRFWSNVFPVFFQFLNIMVVGITGAAVVITILKVFFPVSEYKGILQLDKVDVIPVTAI
NLYPDGPKEKRAENLEDKTCI

Important features of the protein:**Signal peptide:**

amino acids 1-23

Transmembrane domain:

amino acids 266-284

Leucine zipper pattern.

amino acids 155-176

N-glycosylation sites.

amino acids 46-49, 64-67, 166-169, 191-194

FIGURE 23

CGTCTCTGCGTTTCGCCATGCGTCCCCGGGGCGCCAGGGCCACTCTGGCCCTTGCCCTGGGGGG
CCCTGGCTTGGGCCGTGGGCTTCGTGAGCTCCATGGGCTCGGGGAACCCCGGCCCGGTGGT
GTTTGCTGGCTCCAGCAGGGCCAGGAGGCCACCTGCAAGCCTGGTGTCCAGACTGATGTAC
CCGGGCCGAGTGCTGTGCCTCCGGCAACATTGACACCGCCTGGTCCAACCTACCCACCCGG
GGAACAAGATCAACCTCCTCGGCTTCTTGGGCCTTGTCACCTGCCTTCCCTGCAAGATTCTG
TGCGACGGCGTGGAGTGC GGCCCGGGCAAGGCGTGCCGCATGCTGGGGGGCGGCCGCGCTG
CGAGTGC GCGCCGACTGCTCGGGGCTCCCGGCGCGGCTGCAGGTGTGCGGCTCAGACGGCG
CCACCTACCGCGACGAGTGC GAGCTGCGCGCGCGGCTGCCGCGGCCACCCGGACCTGAGC
GTCATGTACCGGGGCCGCTGCCGCAAGTCCTGTGAGCACGTGGTGTGCCCGCGGCCACAGTC
GTGCGTCGTGGACCAGACGGGCAGCGCCCACTGCGTGGTGTGTGCGAGCGCGCCCTGCCCTG
TGCCCTCCAGCCCCGGCCAGGAGCTTTCGGGCAACAACAACGTACCTACATCTCCTCGTG
CACATGCGCCAGGCCACCTGCTTCCTGGGCGGCTCCATCGGCGTGCGCCACGCGGGCAGCTG
CGCAGGCACCCCTGAGGAGCGGCCAGGTGGTGAGTGTGCAGAAGAGGAAGAGAACCTTCGTGT
GAGCCCTGCAGGACAGGCCTGGGCCTGGTGCCCGAGGCCCCCATCATCCCCTGTTATTTATT
GCCACAGCAGAGTCTAATTTATATGCCACGGACACTCTTAGAGCCCGGATTTCGGACCACTT
GGGGATCCCAAGACCTCCCTGACGATATCCTGGAAGGACTGAGGAAGGGAGGCCCTGGGGGCC
GGCTGGTGGGTGGGATAGACCTGCGTTCGGGACACTGAGCGCCTGATTTAGGGCCCTTCTCT
AGGATGCCCCAGCCCTACCTAAGACCTATTGCCGGGAGGATTCCACACTCCGCTCCCTT
TGGGGATAAACCTATTAATTATTGCTACTATCAAGAGGGCTGGGCATTCTCTGCTGGTAATT
CCTGAAGAGGCATGACTGCTTTTCTCAGCCCCAAGCCTCTAGTCTGGGTGTGTACGAGGGT
CTAGCCTGGGTGTGTACGGAGGGTCTAGCCTGGGTGAGTACGGAGGGTCTAGCCTGGGTGAG
TACGGAGGGTCTAGCCTGGGTGAGTACGGAGGGTCTAGCCTGGGTGTGTATGGAGGATCTAG
CCTGGGTGAGTATGGAGGGTCTAGCCTGGGTGAGTATGGAGGGTCTAGCCTGGGTGTGTATG
GAGGGTCTAGCCTGGGTGAGTATGGAGGGTCTAGCCTGGGTGTGTATGGAGGGTCTAGCCTG
GGTGAGTATGGAGGGTCTAGCCTGGGTGTGTACGGAGGGTCTAGTCTGAGTGCGTGTGGGGA
CCTCAGAACACTGTGACCTTAGCCCAGCAAGCCAGGCCCTTCATGAAGGCCAAGAAGGCTGC
CACCATTCCCTGCCAGCCCAAGAACCTCCAGCTTCCCCACTGCCTCTGTGTGCCCTTTGCGT
CCTGTGAAGGCCATTGAGAAATGCCAGTGTGCCCTCTGGGAAAGGGCACGGCCTGTGCTCC
TGACACGGGCTGTGCTTGGCCACAGAACCACCCAGCGTCTCCCCTGCTGCTGTCCACGTGAG
TTCATGAGGCAACGTGCGTGGTCTCAGACGTGGAGCAGCCAGCGGAGCTCAGAGCAGGGC
ACTGTGTCCGGCGGAGCCAAGTCCACTCTGGGGGAGCTCTGGCGGGGACACGGGCCACTGC
TCACCCACTGGCCCCGAGGGGGGTGTAGACGCCAAGACTCACGCATGTGTGACATCCGGAGT
CCTGGAGCCGGGTGTCCAGTGGCACCCTAGGTGCTGCTGCCTCCACAGTGGGGTTTACA
CCCAGGGCTCCTTGGTCCCCACAACCTGCCCCGGCCAGGCCTGCAGACCCAGACTCCAGCC
AGACCTGCCACCCACCAATGCAGCCGGGGCTGGCGACACAGCCAGGTGCTGGTCTTGGG
CCAGTTCTCCACGAGGCTCACCCTCCCTCCATCTGCGTTGATGCTCAGAATCGCCTACC
TGTGCTGCGTGTAAACCACAGCCTCAGACCAGCTATGGGGAGAGGACAACACGGAGGATAT
CCAGCTTCCCGGCTCTGGGGTGAGGAATGTGGGGAGCTTGGGCATCCTCCTCCAGCCTCCTC
CAGCCCCCAGGCAGTGCCTTACCTGTGGTGCCAGAAAAGTGCCCTTAGGTTGGTGGGTCTA
CAGGAGCCTCAGCCAGGCAGCCACCCACCCTGGGGCCTGCCTCACCAGGAATAAAGA
CTCAAGCCATAAAAAAA

24/75

FIGURE 24

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62306

<subunit 1 of 1, 263 aa, 1 stop

<MW: 27663, pI: 6.77, NX(S/T): 2

MRPGAPGPLWPLPWGALAWAVGFVSSMSGGNPAPGGVCWLQQGQEATCSLVLQTDVTRAEC
ASGNIDTAWSNLTHPGNKINLLGFLGLVHCLPCKDSCDGVCEGPGKACRMLGGRPRCECAPD
CSGLPARLQVCGSDGATYRDECELRAARCRGHPDLSVMYRGRCRKSCHEVVCPRPQSCVVDQ
TGSAHCVCVRAAPCPVPSSPGQELCGNNNVTYISSCHMRQATCFLGRSIGVRHAGSCAGTPE
EPPGGESAEEEEENFV

Important features:**Signal peptide:**

amino acids 1-20

N-glycosylation sites.

amino acids 73-77, 215-219

Osteonectin domain proteins.

amino acids 97-130, 169-202

25/75

FIGURE 25

TGCAGAGCTTGTGGAGGCC**ATG**GGGCGCGTCGTCGCGGAGCTCGTCTCCTCGCTGCTGGGGT
TGTGGCTGTTGCTGTGCAGCTGCGGATGCCCGAGGGCGCCGAGCTGCGTGCTCCGCCAGAT
AAAATCGCGATTATTGGAGCCGGAATTGGTGGCAC'TTCAGCAGCCTATTACCTGCGGCAGAA
ATTTGGGAAAGATGTGAAGATAGACCTGTTTGAAGAGAAGAGGTCGGGGGCCGCTGGCTA
CCATGATGGTGCAGGGGCAAGAATACGAGGCAGGAGGTTCTGTCTATCCATCCTTTAAATCTG
CACATGAAACGTTTTTGTCAAAGACCTGGGTCTCTCTGCTGTTTCAGGCCTCTGGTGGCCTACT
GGGGATATATAATGGAGAGACTCTGGTATTTGAGGAGAGCAACTGGTTCATAATTAACGTGA
TTAAATTAGTTTGGCGCTATGGATTTCATCCCTCCGTATGCACATGTGGGTAGAGGACGTG
TTAGACAAGTTCATGAGGATCTACCGCTACCAGTCTCATGACTATGCCTTCAGTAGTGTCGA
AAAATTACTTCATGCTCTAGGAGGAGATGACTTCCTTGAATGCTTAATCGAACACTTCTTG
AAACCTTGCAAAAGGCCGGCTTTTCTGAGAAGTTCCTCAATGAAATGATTGCTCCTGTTATG
AGGGTCAATTATGGCCAAAGCACGGACATCAATGCCTTTGTGGGGCGGTGTCACTGTCCTG
TTCTGATTCTGGCCTTTGGGCAGTAGAAGGTGGCAATAAACTTGTTTGCTCAGGGCTTCTGC
AGGCATCCAAAAGCAATCTTATATCTGGCTCAGTAATGTACATCGAGGAGAAAACAAAGACC
AAGTACACAGGAAATCCAACAAAGATGTATGAAGTGGTCTACCAAATTGGAAC TGAGACTCG
TTCAGACTTCTATGACATCGTCTTGGTGGCCACTCCGTTGAATCGAAAAATGTCGAATATTA
CTTTTCTCAACTTTGATCCTCCAATTGAGGAATCCATCAATATTATCAACATATAGTGACA
ACTTTAGTTAAGGGGAATTGAATACATCTATCTTTAGCTCTAGACCCATAGATAAATTTGG
CCTTAATACAGTTTTAACCACTGATAATTCAGATTGTTCATTAACAGTATTGGGATTGTGC
CCTCTGTGAGAGAAAAGGAAGATCCTGAGCCATCAACAGATGGAACATATGTTTGGAAGATC
TTTTCCCAAGAACTCTTACTAAAGCACAAATTTTAAAGCTCTTTCTGTCTATGATTATGC
TGTGAAGAAGCCATGGCTTGCATATCCTCACTATAAGCCCCCGAGAAATGCCCTCTATCA
TTCTCCATGATCGACTTTATTACCTCAATGGCATAGAGTGTGCAGCAAGTGCCATGGAGATG
AGTGCCATTGCAGCCCACAACGCTGCACTCCTTGCCATACACCGCTGGAACGGGCACACAGA
CATGATTGATCAGGATGGCTTATATGAGAACTTAAACTGAAC'TGAAGTGACACACTCC
TTTTTCCCCTCCTAGTTCCAAATGACTATCAGTGGCAAAAAAGAACAAATCTGAGCAGAGA
TGATTTTGAACCAGATATTTTGCCATTATCATTGTTTAATAAAAGTAATCCCTGCTGGTCAT
AGGAAAAAAAAAAAAA

27/75

FIGURE 27

CATTTCCAACAAGAGCACTGGCCAAGTCAGCTTCTTCTGAGAGAGTCTCTAGAAGACATGAT
GCTACACTCAGCTTTGGGTCTCTGCCTCTTACTCGTCACAGTTTCTTCCAACCTTGCCATTG
CAATAAAAAAGGAAAAGAGGCCTCCTCAGACACTCTCAAGAGGATGGGGAGATGACATCACT
TGGGTACAAACTTATGAAGAAGGTCTCTTTTATGCTCAAAAAAGTAAGAAGCCATTAATGGT
TATTCATCACCTGGAGGATTGTCAATACTCTCAAGCACTAAAGAAAGTATTTGCCCCAAATG
AAGAAATACAAGAAATGGCTCAGAATAAGTTCATCATGCTAAACCTTATGCATGAAACCACT
GATAAGAATTTATCACCTGATGGGCAATATGTGCCTAGAATCATGTTTGTTAGACCCTTCTTT
AACAGTTAGAGCTGACATAGCTGGAAGATACTCTAACAGATTGTACACATATGAGCCTCGGG
ATTTACCCCTATTGATAGAAAACATGAAGAAAGCATTAAAGACTTATTTCAGTCAGAGCTATAA
GAGATGATGGAAAAAGCCTTCACCTCAAAGAAGTCAAATTTTCATGAAGAAAACCTCTGGCA
CATTGACAAATACTAAATGTGCAAGTATATAGATTTTGTAATATTACTATTTAGTTTTTTTA
ATGTGTTTGCAATAGTCTTATTAAAATAAATGTTTTTTAAATCTGA

28/75

FIGURE 28

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64896

<subunit 1 of 1, 166 aa, 1 stop

<MW: 19171, pI: 8.26, NX(S/T): 1

MMLHSALGLCLLLVTVSSNLAIKKEKRPPQTLSRGWGDDITWVQTYEGLFYAQKSKKPL
MVIHHLEDCQYSQALKKVFAQNEEIQEMAQNKFIMLNLMHETTDKNLSPDGQYVPRIMFVDP
SLTVRADIAGRYSNRLYTYEPRDLPLLIENMKKALRLIQSEL

Important features:

Signal peptide:

amino acids 1-23

N-myristoylation site.

amino acids 51-57

29/75

FIGURE 29

TAAACAGCTACAATATTCCAGGGCCAGTCACTTGCCATTTCTCATAACAGCGTCAGAGAGA
AAGAACTGACTGAAACGTTTGAGATGAAGAAAGTTCTCCTCCTGATCACAGCCATCTTGGCA
GTGGCTGTTGGTTTCCCAGTCTCTCAAGACCAGGAACGAGAAAAAGAAGTATCAGTGACAG
CGATGAATTAGCTTCAGGGTTTTTGTGTTCCCTTACCCATATCCATTTGCCCCACTTCCAC
CAATTCATTTCCAAGATTTCCATGGTTTAGACGTAATTTTCCTATTCCAATACCTGAATCT
GCCCCTACAACCTCCCCTTCCTAGCGAAAAGTAAACAAGAAGGATAAGTCACGATAAACCTGG
TCACCTGAAATTGAAATTGAGCCACTTCCTTGAAGAATCAAAATTCCTGTTAATAAAAGAAA
AACAAATGTAATTGAAATAGCACACAGCATTCTCTAGTCAATATCTTTAGTGATCTTCTTTA
ATAACATGAAAGCAAAGATTTTGGTTTCTTAATTTCCACA

FIGURE 30

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71290
><subunit 1 of 1, 85 aa, 1 stop
><MW: 9700, pI: 9.55, NX(S/T): 0
MKKVLLLLITAILAVAVGFVPSQDQEREKRSISDSDELASGFFVFYPYPYFRPLPPIPFPRFP
WFRNRFPIPIPIESAPTTPLPSEK
```

Important features of the protein:

Signal peptide:

amino acids 1-17

Homologous region to B3-hordein:

amino acids 47-85

FIGURE 31

CGGACGCGTGGGCGGGCGCGCCGGGAGGGACCGCGGCGGCATGGGCCGGGGCCCTGGGAT
 GCGGGCCCGTCTCGCCGCTGCTGCCGCTGTTGCTGCTGCTCGGCCCTGGCCCCGGCGCCGC
 GGGAGCGCCGGGCCCGACGGTTTAGACGTCTGTGCCACTTGCCATGAACATGCCACATGCC
 AGCAAAGAGAAGGGAAGAAGATCTGTATTTGCAACTATGGATTGTAGGGAACGGGAGGACT
 CAGTGTGTTGATAAAAAATGAGTGCCAGTTTGGAGCCACTCTTGTCTGGGGAACACACATC
 TTGCCACAACACCCCGGGGGCTTCTATTGCATTGCTGGAAGGATATCGAGCCACAAACA
 ACAACAAGACATTTCATCCCAACGATGGCACCTTTTGTACAGACATAGATGAGTGTGAAGTT
 TCTGGCCTGTGCAGGCATGGAGGGCGATGCGTGAACACTCATGGGAGCTTTGAATGCTACTG
 TATGGATGGATACTTGCCAAGGAATGGACCTGAACCTTTCCACCCGACCACCGATGCCACAT
 TATGCACAGAAATAGACTGTGGTACCCTCCTGAGGTTCCAGATGGCTATATCATAGGAAAT
 TATACGTCTAGTCTGGGCAGCCAGGTTCGTTATGCTTGCAGAGAAGGATTCTTCAGTGTTC
 AGAAGATACAGTTTCAAGCTGCACAGGCCTGGGCACATGGGAGTCCCCAAAATTACATTGCC
 AAGAGATCAACTGTGGCAACCCTCCAGAAATGCGGCACGCCATCTTGGTAGGAAATCACAGC
 TCCAGGCTGGGCGGTGTGGCTCGCTATGTCTGTCAAGAGGGCTTTGAGAGCCCTGGAGGAAA
 GATCACTTCTGTTTGGCACAGAGAAAGGCACCTGGAGAGAAAGTACTTTAACATGCCACAGAAA
 TTCTGACAAAGATTAATGATGTATCACTGTTTAAATGATACCTGTGTGAGATGGCAAATAAAC
 TCAAGAAGAATAAACCCCAAGATCTCATATGTGATATCCATAAAAGGACAACGGTTGGACCC
 TATGGAATCAGTTTCGTGAGGAGACAGTCAACTTGACCACAGACAGCAGGACCCAGAAAGTGT
 GCCTAGCCCTGTACCCAGGCACCAACTACACCGTGAAACATCTCCACAGCACCTCCAGGGCGC
 TCGATGCCAGCCGTCATCGGTTTCCAGACAGCTGAAGTTGATCTCTTAGAAGATGATGGAAG
 TTTCAATATTTCAATATTTAATGAACTTGTTTGAATTTGAACAGGCGTTCTAGGAAAGTTG
 GATCAGAACACATGTACCAATTTACCGTTCTGGGTCAGAGGTGGTATCTGGCTAACTTTTCT
 CATGCAACATCGTTTAACTTCACAACGAGGGAACAGTGCTGTAGTGTGTTTGGATCTGTA
 CCCTACGACTGATTATACGGTGAATGTGACCCTGCTGAGATCTCTTAAGCGGCACTCAGTGC
 AAATAACAATAGCAACTCCCCCAGCAGTAAACAGACCATCAGTAACATTTTCAGGATTTAAT
 GAAACCTGCTTGAGATGGAGAAGCATCAAGACAGCTGATATGGAGGAGATGTATTTATCCCA
 CATTTGGGGCCAGAGATGGTATCAGAAGGAATTTGCCAGGAATGACCTTTAATATCAGTA
 GCAGCAGCCGAGATCCCGAGGTGTGCTTGGACCTACGTCGGGTACCAACTACAAATGTCACT
 CTCCGGGCTCTGTCTTCGGAACCTTCTGTGGTCACTCTCCCTGACAACCCAGATAACAGAGCC
 TCCCTCCCGGAAGTAGAATTTTTTACGGTGCACAGAGGACCTCTACCACGCCTCAGACTGA
 GGAAGCCCAAGGAGAAAAATGGACCAATCAGTTCATATCAGGTGTTAGTGCTTCCCTGGCC
 CTCCAAAGCACATTTTCTTGATGATTCTGAAGGCGCTTCTCCTTCTTTAGCAACGCCTCTGA
 TGCTGATGGATACGTGGCTGCAGAACTACTGGCCAAAGATGTTCCAGATGATGCCATGGAGA
 TACCTATAGGAGACAGGCTGTACTATGGGGAATATTATATGACCCGTTGAAAAGAGGGAGT
 GATTACTGCATTATATTACGAATCACAAGTGAATGGAATAAGGTGAGAAGACACTCCTGTGC
 AGTTTGGGCTCAGGTGAAAGATTCTGCTACTCATGCTGCTGCAGATGGCGGGGTGTTGGACTGG
 GTTCCCTGGCTGTGTGATCATTCTCACATTCTCCTCTCCTCAGCGGTGTGATGGCAGATG
 GACACTGATGGGGAGGATGCACTGCTGCTGGGCAGGTGTTCTGGCAGCTTCTCAGGTGCC
 GCACAGAGGCTCCGTGTGACTTCCGTCCAGGGAGCATGTGGGCCTGCAACTTTCTCCATTCC
 CAGCTGGGCCCCATTCTGGATTAAAGATGGTGGCTATCCCTGAGGAGTCACCATAAGGAGA
 AAACCTCAGGAATTTCTGACTTCTCCCTGCTACAGGACAGTTCTGTGCAATGAACCTTGAGACT
 CCTGATGTACACTGTGATATTGACCGAAGGCTACATACAGATCTGTGAATCTTGGCTGGGAC
 TTCCTCTGAGTGATGCCTGAGGGTCAGCTCCTCTAGACATTGACTGCAAGAGAATCTCTGCA
 ACCTCCTATATAAAGCATTTCTGTTAATTATTCAAGATCCATTCTTTACAATATGCAAGTG
 AGATGGGCTTAAGTTTGGGCTAGAGTTTGACTTTATGAAGGAGGTCAATGAAAAAGAGAACA
 GTGACGTAGGCAAAATGTTCAAGCACTTTAGAAACAGTACTTTTCTATAAATTAGTTGATAT
 ACTAATGAGAAAAATACTAGCCTGGCCATGCCAATAAGTTTCTGCTGTGTCTGTAGGCA
 GCATTGCTTTGATGCAATTTCTATTGTCCTATATATTCAAAAGTAATGCTACATTTCCAGTA
 AAAATATCCCGTAATTAAAAA

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FIGURE 32

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96031
><subunit 1 of 1, 747 aa, 1 stop
><MW: 82710, pI: 6.36, NX(S/T): 18
MGRGPWDAGPSRRLLPLLLLLGLARGAAGAPGPDGLDVCATCHEHATCQQREGKKICICNYG
FVGNGRTQCVDKNECQFGATLVCGNHTSCHNTPGGFYCICLEGYRATNNNKTFFPNDGTFCT
DIDECEVSGLCRHGGRCVNTHGSFECYCMDGYLPRNGPEPFHPTTATSCTEIDCGTPPEVP
DGYIIGNYTSSLGSQVRYACREGFFSVPEDTVSSCTGLGTWESPKLHCQEINCGNPPEMRHA
ILVGNHSSRLGGVARYVCQEGFESPGGKITSVCTEKG TWRESTLTCTEILTKINDVSLFNDT
CVRWQINSRRINPKISYVISIKGQRLDPMESVREETVNLTTDSRTEPVCLALYPGTNYTVNI
STAPRRRSMFAVIGFQTAEDVLLEDDGSFNISIFNETCLKLNRRSRKVGSEHMYQFTVLGQR
WYLANFHSATSFNFTTREQVPVVCLDLYPTTDYTVNVTLLRSPKRHSVQITITATPPAVKQTI
SNISGFNETCLRWRISIKTADMEEMYLFIHWQQRWYQKEFAQEMTFNISSSSRDPEVCLDLRP
GTNYNVSLRALSSELPPVISLTTQITEPPLPEVEFFT VHRGGLPRLRLRKAKEKNGPISSYQ
VLVPLALQSTFSCDSEGFSSNASDADGYVAAELLAKDVPDDAMEIPIGDRLYYGEYYN
APLKRGSDYCIILRITSEWNKVRHSCAVWAQVKDSSLMLLQMAGVGLGSLAVVIILTLFLSF
SAV
```

Important features of the protein:**Signal peptide:**

amino acids 1-29

Transmembrane domain:

amino acids 718-740

N-glycosylation sites.

amino acids 87-91, 112-116, 193-197, 253-257, 308-312, 348-352,
367-371, 371-375, 402-406, 407-411, 439-443, 447-451, 470-474,
498-502, 503-507, 542-546, 563-567, 645-649

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 478-482, 686-690, 705-709

Tyrosine kinase phosphorylation site.

amino acids 419-427

N-myristoylation sites.

amino acids 22-28, 35-41, 65-71, 86-92, 96-102, 120-126,
146-152, 192-198, 252-258, 274-280, 365-371, 559-565, 688-694,
727-733.

Amidation site.

amino acids 52-56

Aspartic acid and asparagine hydroxylation sites.

amino acids 91-103, 141-153.

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 624-635

Cytochrome c family heme-binding site signature.

amino acids 39-45

Calcium-binding EGF-like domain proteins pattern proteins.

amino acids 85-106, 135-156

Receptor tyrosine kinase class V proteins:

amino acids 389-422

FIGURE 33

GGAAAAGGTACCCGCGAGAGACAGCCAGCAGTTCTGTGGAGCAGCGGTGGCCGGCTAGG**ATG**
GGCTGTCTCTGGGGTCTGGCTCTGCCCTTTTCTTCTTCTGCTGGGAGGTTGGGGTCTCTGG
GAGCTCTGCAGGCCCCAGCACCCGAGAGCAGACACTGCGATGACAACGGACGACACAGAAG
TGCCCGCTATGACTCTAGCACCGGGCCACGCCGCTCTGGAAACTCAAACGCTGAGCGCTGAG
ACCTCTTCTAGGGCCTCAACCCAGCCGGCCCCATTCCAGAAGCAGAGACCAGGGGAGCCAA
GAGAATTTCCCCTGCAAGAGAGACCAGGAGTTTCACAAAACATCTCCCAACTTCATGGTG
TGATCGCCACCTCCGTGGAGACATCAGCCGCCAGTGGCAGCCCCGAGGGAGCTGGAATGACC
ACAGTTCAGACCATCACAGGCAGTGATCCCAGGAAGCCATCTTTGACACCTTTGCACCGA
TGACAGCTCTGAAGAGGCCAAAGACACTCACAATGGACATATTGACATTGGCTCACACCTCCA
CAGAAGCTAAGGGCCTGTCTCTCAGAGAGCAGTGCCCTCTTCCGACGGCCCCCATCCAGTCATC
ACCCCGTCACGGGCCTCAGAGAGCAGCGCCTCTTCCGACGGCCCCCATCCAGTCATCACCCC
GTCACGGGCCTCAGAGAGCAGCGCCTCTTCCGACGGCCCCCATCCAGTCATCACCCCGTCAT
GGTCCCGGGATCTGATGTCACTCTCTCGCTGAAGCCCTGGTGACTGTCAAAACATCGAG
GTTATTAATTGCAGCATCACAGAAATAGAAACAACAACCTTCAGCATCCCTGGGGCCTCAGA
CATAGATCTCATCCCCACGGAAGGGGTGAAGGCCTCGTCCACCTCCGATCCACCAGCTCTGC
CTGACTCCACTGAAGCAAAACCACACATCACTGAGGTCACAGCCTCTGCCGAGACCCTGTCC
ACAGCCGGCACCACAGAGTCAGCTGCACCTCATGCCACGGTTGGGACCCCACTCCCCACTAA
CAGCGCCACAGAAAGAGAAGTGACAGCACCCGGGGCCACGACCCTCAGTGGAGCTCTGGTCA
CAGTTAGCAGGAATCCCCTGGAAGAAACCTCAGCCCTCTCTGTTGAGACACCAAGTTACGTC
AAAGTCTCAGGAGCAGCTCCGGTCTCCATAGAGGCTGGGTACAGCAGTGGGCAAAACAACCTC
CTTTGCTGGGAGCTCTGCTTCTCTCTACAGCCCCCTCGGAAGCCGCCCTCAAGAACTTCACCC
CTTCAGAGACACCGACCATGGACATCGCAACCAAGGGGCCCTTCCCCACCAGCAGGGACCCT
CTTCCTTCTGTCCCTCCGACTACAACCAACAGCAGCCGAGGGACGAACAGCACCTTAGCCAA
GATCACAACTCAGCGAAGACCACGATGAAGCCCCAACAGCCACGCCACGACTGCCCGGAC
GAGGCCGACCACAGACCT**CGA**GTGCAGGTGAAAATGGAGGTTTCCTCCTCTGCGGCTGAGTG
TGGCTTCCCCGGAAGACCTCACTGACCCAGAGTGGCAGAAAGGCTGATGCAGCAGCTCCAC
CGGGAACCTCACGCCACGCGCCTCACTCCAGGTCTCCTTACTGCGGTGCAGGAGAGGCTA
ACGGACATCAGCTGCAGCCAGGCATGTCCCGTATGCCAAAAGAGGGTGCTGCCCTAGCCTG
GGCCCCACCGACAGACTGCAGCTGCGTTACTGTGCTGAGAGGTACCCAGAAGGTTCCCATG
AAGGGCAGCATGTCCAAGCCCCTAACCCAGATGTGGCAACAGGACCCTCGCTCACATCCAC
CGGAGTGATGTATGGGGAGGGGCTTACCTGTTCCAGAGGTGTCCTTGGACTCACCTTGG
CACATGTTCTGTGTTTCAGTAAAGAGAGACCTGATCACCCATCTGTGTGCTTCCATCCTGCA
TTAAATTCACCTCAGTGTGGCCCAAAAAA

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FIGURE 34

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108722
><subunit 1 of 1, 482 aa, 1 stop
><MW: 49060, pI: 4.74, NX(S/T): 4
MGCLWGLALPLFFFCWEVGVSGSSAGPSTRRADTAMTTDDTEVPAMTLAPGHAALETQTLA
ETSSRASTPAGPIPEAETRGAKRISPARETRSFTKTSNFMVLIATSVETSAASGSPEGAGM
TTVQITITGSDPEEAFDITLCTDDSSSEEAKTLTMDILTLAHTSTEAKGLSSESSASSDGPHPV
ITPSRASESSASSDGPHPVITPSRASESSASSDGPHPVITPSWSPGSDVTLLEALVTVTNI
EVINCSITEIETTTSSIPGASDIDLIPTEGVKASSTSDPPALPDSTEAKPHITEVTASAETL
STAGTTESAAPHATVGTPLPTNSATEREVTAPGATTLGALVTVSRNPLEETSALSVETPSY
VKVSGAAPVSI EAGSAVGKTTSFAGSSASSYSPSEAALKNFTPSETPTMDIATKGFPTSRD
PLPSVPPTTTNSSRGTNSTLAKITTSAKTTMKPQQPRPRLPGRGRPQT

```

Important features of the protein:**Signal peptide:**

amino acids 1-25

N-glycosylation sites.

amino acids 252-256, 445-449, 451-455

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 84-88

N-myristoylation sites.amino acids 2-8, 19-25, 117-123, 121-127, 232-238, 278-284,
314-320, 349-355, 386-392, 397-403, 449-455**ATP/GTP-binding site motif A (P-loop).**

amino acids 385-393

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FIGURE 35

GCCTCTGAATTGTTGGGCAGTCTGGCAGTGGAGCTCTCCCCGGTCTGACAGCCACTCCAGAG
GCCATGCTTCGTTTCTTGCCAGATTGGCTTTCAGCTTCCTGTTAATTCTGGCTTTGGGCCA
GGCAGTCCAATTTCAAGAATATGTCTTCTCCAATTTCTGGGCTTAGATAAGGCGCCTTCAC
CCCAGAAGTTC AACCTGTGCCTTATATCTTGAAGAAAATTTTCAGGATCGCGAGGCAGCA
GCGACCACTGGGGTCTCCCGAGACTTATGCTACGTAAAGGAGCTGGGCGTCCGCGGGAATGT
ACTTCGCTTTCTCCAGACCAAGGTTCTTTCTTTACCCAAAGAAAATTTCCCAAGCTTCCT
CCTGCCTGCAGAAGCTCCTCTACTTTAACCTGTCTGCCATCAAAGAAAGGGAACAGTTGACA
TTGGCCCAGCTGGGCCTGGACTTGGGGCCCAATTCTTACTATAACCTGGGACCAGAGCTGGA
ACTGGCTCTGTTCTGGTTCAGGAGCCTCATGTGTGGGGCCAGACCACCCCTAAGCCAGGTA
AAATGTTTGTGTTGCGGTCACTCCCATGGCCACAAGGTGCTGTTCACTTCAACCTGCTGGAT
GTAGCTAAGGATTGGAATGACAACCCCCGGAAAAATTTCTGGGTTATTCTTGAGATACTGGT
CAAAGAAGATAGAGACTCAGGGGTGAATTTTCAGCCTGAAGACACCTGTGCCAGACTAAGAT
GCTCCCTTCATGCTTCCCTGCTGGTGGTGACTCTCAACCCTGATCAGTGCCACCCTTCTCGG
AAAAGGAGAGCAGCCATCCCTGTCCCCAAGCTTTCTTGTAAGAACCCTGTGCCACCGTCACCA
GCTATTTCATTAACCTCCGGGACCTGGGTTGGCACAAGTGGATCATTGCCCCAAGGGGTTCA
TGGCAAATTACTGCCATGGAGAGTGTCCCTTCTCACTGACCATCTCTCAACAGCTCCAAT
TATGCTTTCATGCAAGCCCTGATGCATGCCGTTGACCCAGAGATCCCCCAGGCTGTGTGTAT
CCCCACCAAGCTGTCTCCCATTTCCATGCTCTACCAGGACAATAATGACAATGTCATTCTAC
GACATTATGAAGACATGGTAGTCGATGAATGTGGGTGTGGGTTAGGATGTCAGAAATGGGAAT
AGAAGGAGTGTTCTTAGGGTAAATCTTTTAATAAAACTACCTATCTGGTTTATGACCACTTA
GATCGAAATGTC

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FIGURE 36

MLRFLPDLAFSFLILALGQAVQFQEYVFLQFLGLDKAPSPQKFQVPYILKKIFQDREAAA
 TTGVSRLCYVKELGVRGNVLRFLPDQGFFLYPKKISQASSCLQKLLYFNLSAIKEREQLTL
 AQLGLDLGPNSYYNLGFELELALFLVQEPHVWGQTTPKPGKMFVLRVWPWPQGAVHFNLLDV
 AKDWNNDNPRKNFGLFLEILVKEDRDSGVNFQPEDTCARLRCSLHASLLVVTLNPDQCHPSRK
 RRAAIPVVKLSCKNLCHRHQLFINFRDLGWHKWIIAPKGFMANYPCHGECPFSLTISLNSSNY
 AFMQALMHAVDPEIPQAVCIPTKLSPISMLYQDNNNDNVILRHYEDMVVDECGCG

Important features of the protein:

Signal peptide:

amino acids 1-21

N-glycosylation sites.

amino acids 112-116, 306-310

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 96-100

N-myristoylation site.

amino acids 77-83

TGF-beta family proteins.

amino acids 264-299, 327-341, 345-364

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FIGURE 37

CACTTTCTCCCTCTCTTCTTTACTTTTCGAGAAACCGCGCTTCCGCTTCTGGTCGCAGAGAC
 CTCGGAGACCGCGCCGGGGAGACGGAGGTGCTGTGGGTGGGGGGGACCTGTGGCTGCTCGTA
 CCGCCCCCACCTCTCTTCTGCACTGCCGTCTCCGGAAGACCTTTTCCCTGCTCTGTT
 TCCTTCACCGAGTCTGTGCATCGCCCCGGACCTGGCCGGGAGGAGCTTGGCCGGCGGGAGA
 TGCTCTAGGGGCGCGCCGGGAGGAGCGGCCGGCGGACGGAGGGCCCGGAGGAAGATGGGGC
 TCCCGTGGACAGGGACTCTTGCTGGCGTACTGCCTGCTCCTTGCCCTTGGCTCTGGCCTGGT
 CCTGAGTCGTGTGCCCCATGTCCAGGGGGAACAGCAGGAGTGGGAGGGGACTGAGGAGCTGC
 CGTCGCCTCCGACCATGCCGAGAGGGCTGAAGAACAACATGAAAAATACAGGCCAGTCAG
 GACCAGGGGCTCCCTGCTTCCCGGTGCTTGCGCTGCTGTGACCCCGGTACCTCCATGTACCC
 GGCGACCGCCGTGCCCCAGATCAACATCACTATCTTGAAAGGGGAGAAGGGTGACCGCGGAG
 ATCGAGGCCCTCCAAGGGAAATATGGCAAAACAGGCTCAGAGGGGCCAGGGGCCACACTGGA
 CCCAAAGGGCAGAAGGGCTCCATGGGGGCCCCCTGGGGAGCGGTGCAAGAGCCACTACGCCGC
 CTTTTCGGTGGGCGCGAAGAAGCCATGACACAGCAACCACTACTACCAGACGGTGATCTTCG
 ACACGGAGTTCGTGAACCTCTACGACCACTTCAACATGTTACCCGGCAAGTTCTACTGCTAC
 GTGCCCGGCTCTACTTCTTCAGCCTCAACGTGCACACCTGGAACCCAGAAGGACCTACCT
 GCACATCATGAAGAACGAGGAGGAGGTGGTGATCTTGTTGCGCAGGTGGGCGACCGCAGCA
 TCATGCAAAGCCAGAGCCTGATGCTGGAGCTGCGAGAGCAGGACCAGGTGTGGGTACGCCTC
 TACAAGGGCGAACGTGAGAACGCCATCTTCAGCGAGGAGCTGGACACCTACATCACTTTCAG
 TGGCTACCTGGTCAAGCACGCCACCGAGCCCCTAGCTGGCCGGCCACCTCCTTTCTCTCGCC
 ACCTTCCACCCCTGGCTGTGCTGACCCACCGCCTCTTCCCGATCCCTGGACTCCGACTC
 CTTGGCTTTGGCATTTCAGTGAGCGCCTGCACACACAGAAAGCCAGAGCCATCGGTCTCC
 CAGATCCCGCAGCCTCTGGAGAGAGCTGACGGCAGATGAAATCACCAGGGCGGGGCACCCGC
 GAGAACCCCTCTGGGACCTTCCGCGGCCCTCTCTGCACACATCCTCAAGTGACCCCGCACGGC
 GAGACGCGGTGGCGCGAGGGCTCCAGGGTGCGGCACCGCGGCTCCAGTCCCTTGGAATA
 ATTAGGCAAATTTCTAAAGGTCTCAAAGGAGCAAAGTAAACCGTGGAGGACAAAGAAAGGG
 TTGTTATTTTTGTCTTCCAGCCAGCCTGCTGGCTCCCAAGAGAGAGGCCCTTTTCAGTTGAG
 ACTCTGCTTAAGAGAAGATCCAAAGTTAAAGCTCTGGGGTCAGGGGAGGGGCCGGGGCAGG
 AAACCTACCTCTGGCTTAATTTCTTTAAGCCACGTAGGAACCTTTCTGAGGGATAGGTGGACC
 CTGACATCCCTGTGGCTTGCCCAAGGGCTCTGCTGGTCTTTCTGAGTCACAGCTGCGAGGT
 GATGGGGGCTGGGGCCCCAGGCGTCAGCCTCCCAGAGGGACAGCTGAGCCCCCTGCCTTGGC
 TCCAGGTTGGTAGAAGCACGCCAAGGGCTCCTGACAGTGCCAGGGACCCCTGGGTCCCCCA
 GGCCTGCAGATGTTTCTATGAGGGGCAGAGCTCCTTGGTACATCCATGTGTGGCTCTGCTCC
 ACCCTGTGCCACCCAGAGCCCTGGGGGGTGGTCTCCATGCTGCCACCTGGCATCGGCT
 TTCTGTGCGCCTCCCAACAATCAGCCCCAGAAGGCCCGGGGCTTGGCTCTGTTTTT
 TATAAAACACCTCAAGCAGCACTGCAGTCTCCCATCTCCTCGTGGGCTAAGCATCACCGCTT
 CCACGTGTGTTGTGTGTGGTTGGCAGCAAGGCTGATCCAGACCCCTTCTGCCCCACTGCCCCT
 CATCCAGGCCTCTACCACTAGCCTGAGAGGGGCTTTTCTAGGCTTCAGAGCAGGGGAGAG
 CTGGAAGGGGCTAGAAAGCTCCCGCTTGTCTGTTCTCAGGCTCCTGTGAGCCTCAGTCCGT
 AGACCAGAGTCAAGAGGAAGTACACGTCCCAATCACCCGTGTCAAGATTCACTCTCAGGAGC
 TGGGTGGCAGGAGAGGCAATAGCCCCCTGTGGCAATTGCAGGACCAGCTGGAGCAGGGTTGCG
 GTGCTCCACGGTGCTCTCGCCCTGCCCATGGCCACCCAGACACTGTGATCTCCAGGAACCCC
 ATAGCCCCCTCTCCACCTCACCCCATGTTGATGCCCAGGGTCACTCTTGCTACCCGCTGGGCC
 CCAAACCCCGCTGCCTCTCTTCTTCCCCCATCCCCACCTGGTTTTGACTAACTCTGCT
 TTCCCTCTCTGGGCTGGCTGCGCGGAGTCTGGGTCCCTAAGTCCCTCTCTTTAAAGAACTT
 CTGCGGGTCAGACTCTGAAGCCGAGTTGCTGTGGGCGTGCCCGGAAGCAGAGCGCCACACTC
 GCTGCTTAAGCTCCCCAGCTCTTCCAGAAAACATTAAACTCAGAATTGTGTTTTCAA

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FIGURE 39

GAATTCGGCACGAGGGAAGAAGAGAAAGAAAATCTCCGGGGCTGCTGGGAGCATATAAAGAA
GCCCTGTGGCCTTGCTGGTTTTACCATCCAGACCAGAGTCAGGCCACAGACGGAC**ATG**GCTG
CTCAAGGCTGGTCCATGCTCCTGCTGGCTGTCTTAACCTAGGCATCTTCGTC CGTCCCTGT
GACACTCAAGAGCTACGATGTCTGTGTATTTCAGGAACACTCTGAATTCATTCCTCTCAA
ACTCATTAATAATATAATGGTGATATTCGAGACCATTACTGCAACAGAAAGGAAGTGATAGCAG
TCCCAAAAAATGGGAGTATGATTTGTTTGGATCCTGATGCTCCATGGGTGAAGGCTACTGTT
GGCCAATTACTAACAGGTTCCCTACCTGAGGACCTCAAACAAAAGGAATTTCCACCGGCAAT
GAAGCTTCTGTATAGTGTTGAGCATGAAAAGCCTCTATATCTTTCATTTGGGAGACCTGAGA
ACAAGAGAATATTTCCCTTTCCAATTCGGGAGACCTCTAGACACTTTGCTGATTTAGCTCAC
AACAGTGATAGGAATTTTCTACGGGACTCCAGTGAAGTCAGCTTGACAGGCAGTGATGCC**TA**
AAAGCCACTCATGAGGCAAAGAGTTTCAAGGAAGCTCTCCTCCTGGAGTTTGGCGTTCTCA
TTCTTATACTCTATTCCCGCGTTAGTCTGGTGTATGGATCTATGAGCTCTCTTTTAATATTT
TATTATAAATGTTTTATTTACTTAACTTCCTAGTGAATGTTACAGGTGACTGCTCCCCCAT
CCCCATTTCTTGATATTACATATAATGGCATCATATACCCCTTTATTGACTGACAAACTACT
CAGATTGCTTAACATTTTGTGCTTCAAAGTCTTATCCCACTCCACTATGGGCTGTTACAGAG
TGCATCTCGGTGTAGAGCAAGGCTCCTTGCTTCAGTGCCCCAGGGTGAAATACTTCTTTGA
AAAATTTTCATTCATCAGAAAATCTGAAATAAAAAATATGTCCTTAATTGAG

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FIGURE 40

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73838

><subunit 1 of 1, 167 aa, 1 stop

><MW: 19091, pI: 7.48, NX(S/T): 1

MAAQGWSMLLLAVLNIGIFVRPCDTQELRCLCIQEHSEFIPLKLIKIMVIFETIYCNRKEV
IAVPKNGSMICLDPDAPWVKATVGPITNRFLPEDLKQKEFPPAMKLLYSVEHEKPLYLSFGR
PENKRIFPFPIRETSRHFADLAHNSDRNFLRDSSEVSLTGSDA

Important features of the protein:**Signal peptide:**

amino acids 1-25

N-glycosylation site.

amino acids 68-72

N-myristoylation site.

amino acids 69-75

Small cytokines (intercrine/chemokine) C-x-C subfamily signature

amino acids 40-85

FIGURE 41

CAGACATGGCTCAGTCACTGGCTCTGAGCCTCCTTATCCTGGTTCTGGCCTTTGGCATCCCC
AGGACCCAAGGCAGTGATGGAGGGGCTCAGGACTGTTGCCTCAAGTACAGCCAAAGGAAGAT
TCCCGCCAAGGTTGTCCGCAGCTACCGGAAGCAGGAACCAAGCTTAGGCTGCTCCATCCCAG
CTATCCTGTTCTTGCCCCGCAAGCGCTCTCAGGCAGAGCTATGTGCAGACCCAAGGAGCTC
TGGGTGCAGCAGCTGATGCAGCATCTGGACAAGACACCATCCCCACAGAAACCAGCCCAGGG
CTGCAGGAAGGACAGGGGGGCCTCCAAGACTGGCAAGAAAGGAAAGGGCTCCAAAGGCTGCA
AGAGGACTGAGCGGTCACAGACCCCTAAAGGGCCATAGCCCAGTGAGCAGCCTGGAGCCCTG
GAGACCCACCCAGCCTCACCAGCGCTGAAGCCTGAACCCAAGATGCAAGAAGGAGGCTATG
CTCAGGGGCCCTGGAGCAGCCACCCCATGCTGGCCTTGCCACACTCTTTCTCCTGCTTTAAC
CACCCCATCTGCATTCCCAGCTCTACCCCTGCATGGCTGAGCTGCCCACAGCAGGCCAGGTCC
AGAGAGACCGAGGAGGGAGAGTCTCCAGGGAGCATGAGAGGAGGCAGCAGGACTGTCCCCT
TGAAGGAGAATCATCAGGACCCTGGACCTGATACGGCTCCCCAGTACCCCCACCTCTTCCT
TGTAATATGATTTATACCTAACTGAATAAAAAGCTGTTCTGTCTTCCNCCCA

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FIGURE 42

><MW: 14646, pI: 10.45, NX(S/T): 0

MAQSLALSLILVLAFGIPRTQGSDGGAQDCCLKYSQRKIPAKVVRSYRKQEPSLGCSIPAI
LFLPRKRSQAELCADPKELWVQQLMQHLDKTPSPQKPAQGCRKDRGASKTGKKKGSGKGCKR
TERSQTPKGP

Important features of the protein:

Signal peptide:

amino acids 1-17

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 67-71

N-myristoylation sites.

amino acids 17-23, 23-29, 27-33, 108-114, 118-124, 121-127

Amidation site.

amino acids 112-116

Small cytokines.

amino acids 51-91

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FIGURE 43

AAGGAGCAGCCCGCAAGCACCAAGTGAGAGGCATGAAGTTACAGTGTGTTTCCCTTTGGCTC
CTGGGTACAATACTGATATTGTGCTCAGTAGACAACCACGGTCTCAGGAGATGTCTGATTTT
CACAGACATGCACCATATAGAAGAGAGTTTCCAAGAAATCAAAAGAGCCATCCAAGCTAAGG
ACACCTTCCCAAATGTCACATATCCTGTCCACATTGGGAGACTCTGCAGATCATTAAGCCCTTA
GATGTGTGCTGCGTGACCAAGAACCTCCTGGCGTTCTACGTGGACAGGGTGTTCAAGGATCA
TCAGGAGCCAAACCCCAAAATCTTGAGAAAAATCAGCAGCATTGCCAACTCTTTCCTCTACA
TGCAGAAAACCTCTGCGGCAATGTCAGGAACAGAGGCAGTGTCAGTGCAGGCAGGAAGCCACC
AATGCCACCAGAGTCATCCATGACAACTATGATCAGCTGGAGGTCCACGCTGCTGCCATTAA
ATCCCTGGGAGAGCTCGACGTCTTTCTAGCCTGGATTAATAAGAATCATGAAGTAATGTTCT
CAGCTTGATGACAAGGAACCTGTATAGTGATCCAGGGATGAACACCCCTGTGCGGTTTACT
GTGGGAGACAGCCACCTTGAAGGGGAAGGAGATGGGGAAGGCCCTTGACAGCTGAAAGTCC
CACTGGCTGGCCTCAGGCTGTCTTATTCGCTTGAAAATAGGCAAAAAGTCTACTGTGGTAT
TTGTAATAAACTCTATCTGCTGAAAGGGCCTGCAGGCCATCCTGGGAGTAAAGGGCTGCCTT
CCCATCTAATTTATTGTAAAGTCATATAGTCCATGTCTGTGATGTGAGCCAAGTGATATCCT
GTAGTACACATTGTACTGAGTGGTTTTTCTGAATAAATCCATATTTTACCTATGA

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FIGURE 44

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA92282
><subunit 1 of 1, 177 aa, 1 stop
><MW: 20452, pI: 8.00, NX(S/T): 2
MKLQCVSLWLLGTILILCSVDNHGLRRCLISTDMHHIEESFQEIKRAIQAKDTFPNVTILST
LETLQIIKPLDVCCVTKNLLAFYVDRVFKDHQEPNPKILRKISSIANSFLYMQKTLRQCQEQ
RQCHCRQEATNATRVIHNDNYDQLEVHAAAIKSLGELDVFLAWINKNHEVMFSA
```

Signal sequence:

amino acids 1-18

N-glycosylation sites.

amino acids 56-60, 135-139

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 102-106

N-myristoylation site.

amino acids 24-30

Actinin-type actin-binding domain signature 1.

amino acids 159-169

FIGURE 45

GCTCCCAGCCAAAGAACCTCGGGGCCGCTGCGCGGTGGGGAGGAGTTCCCCGAAACCCGGCCG
CTAAGCGAGGCCTCCTCCTCCCGCAGATCCGAACGGCCTGGGGCGGGGTCAACCCGGCTGGGA
CAAGAAGCCGCCGCCTGCCTGCCCGGGCCCGGGGAGGGGGCTGGGGCTGGGGCCGGAGGCGG
GGTGTGAGTGGGTGTGTGCGGGGGGGCGGAGGCTTGATGCAATCCCCGATAAGAAATGCTCGGG
TGTCTTGGGCACCTACCCGTGGGGCCCCGTAAGGCGCTACTATATAAGGCTGCCGGCCGGAG
CCGCCGCGCGCTCAGAGCAGGAGCGCTGCGTCCAGGATCTAGGGCCACGACCATCCCAACCC
GGCACTCACAGCCCCGAGCGCATCCCGGTGCGCGCCAGCCTCCCGCACCCCCATCGCCGG
AGCTGCGCCGAGAGCCCCAGGGAGGTGCCATGCGGAGCGGGTGTGTGGTGGTCCACGTATGG
ATCCTGGCCGGCCTCTGGCTGGCCGTGGCCGGGCGCCCCCTCGCCTTCTCGGACGCGGGGCC
CCACGTGCACTACGGCTGGGGCGACCCCATCCGCCTGCGGCACCTGTACACCTCCGGCCCCC
ACGGGCTTCCAGCTGCTTCTTGCGCATCCGTGCCGACGGCGCTGTGGACTGCGCGCGGGGC
CAGAGCGCGCACAGTTTGTGAGAGATCAAGGCAGTCGCTCTGCGGACCGTGGCCATCAAGGG
CGTGACACAGCGTGCGGTACCTCTGCATGGCGCCGACGGCAAGATGCAGGGGCTGCTTCAGT
ACTCGGAGGAAGACTGTGCTTTCGAGGAGGAGATCCGCCCAGATGGCTACAATGTGTACCGA
TCCGAGAAGCACCGCCTCCCGGTCTCCCTGAGCAGTGCCAAACAGCGGCAGCTGTACAAGAA
CAGAGGCTTTCTTCCACTCTCTCATTTCTGCCCATGCTGCCCATGGTCCCAGAGGAGCCTG
AGGACCTCAGGGGCCACTTGGAATCTGACATGTTCTCTTCGCCCCCTGGAGACCGACAGATG
GACCCATTTGGGCTTGTACCCGGACTGGAGGCCGTGAGGAGTCCAGCTTTGAGAAGTAACT
GAGACCATGCCCGGGCCTCTTCACTGCTGCCAGGGGCTGTGGTACCTGCAGCGTGGGGGACG
TGCTTCTACAAGAACAGTCCTGAGTCCACGTTCTGTTTAGCTTTAGGAAGAAACATCTAGAA
GTTGTACATATTAGAGTTTTCCATTGGCAGTGCCAGTTTCTAGCCAATAGACTTGTCTGAT
CATAACATTGTAAGCCTGTAGCTTGCCAGCTGCTGCCTGGGCCCCCATTCTGCTCCCTCGA
GGTTGCTGGACAAGCTGCTGCACTGTCTCAGTTCTGCTTGAATACCTCCATCGATGGGGAAC
TCACTTCCTTTGGAAAAATCTTATGTCAAGCTGAAATCTCTAATTTTTTCTCATCACTTC
CCCAGGAGCAGCCAGAAGACAGGCAGTAGTTTTAATTTAGGAACAGGTGATCCACTCTGTA
AAACAGCAGGTAAATTTCACTCAACCCCATGTGGGAATTGATCTATATCTCTACTTCCAGGG
ACCATTGGCCTTCCCAAATCCCTCCAGGCCAGAACTGACTGGAGCAGGCATGGCCCCACGAG
GCTTCAGGAGTAGGGGAAGCCTGGAGCCCCACTCCAGCCCTGGGACAACCTGAGAATTCCCC
CTGAGGCCAGTTCTGTCTATGGATGCTGTCTGAGAATAACTTGCTGTCCCGGTGTCACTGCT
TTCCATCTCCCAGCCCACCAGCCCTCTGCCACCTCACATGCCTCCCCATGGATTGGGGCCT
CCCAGGCCCCCACCTTATGTCAACCTGCACTTCTTGTTCAAAAATCAGGAAAAGAAAAGAT
TTGAAGACCCCAAGTCTTGTCAATAACTTGCTGTGTGGAAGCAGCGGGGGAAGACCTAGAAC
CCTTTCCCCAGCACTTGGTTTTCCAACATGATATTTATGAGTAATTTATTTTGTATATGTACA
TCTCTTATTTTCTTACATTTATTTATGCCCCCAATTATTTATGTATGTAAGTGAGGTTTG
TTTTGTATATTAAAATGGAGTTTGTTTGT

FIGURE 47

GTCTGTTCCAGGAGTCC TTCGGCGGCTGTTGTGTCA GTGGCCTGATCGCGATGGGACAAA
GGCGCAAGTCGAGAGGAACTGTTGTGCCTCTTCATATTGGCGATCCTGTTGTGTCCCTGG
CATTGGGCAGTGTTACAGTGCACCTCTCTGAACCTGAAGTCAGAATTCCTGAGAATAATCCT
GTGAAGTTGTCTGTGCC TACTCGGGCTTTTCTTCTCCCCGTGTGGAGTGGAAGTTTGACCA
AGGAGACACCACCAGACTCGTTTGCTATAATAACAAGATCACAGCTTCCTATGAGGACCGG
TGACCTTCTTGCCAACTGGTATCACCTTCAAGTCCGTGACACGGGAAGACACTGGGACATAC
ACTTGTATGGTCTCTGAGGAAGGCGGCAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGT
GCTTGTGCCTCCATCCAAGCCTACAGTTAACATCCCCCTCTGCCCACCATTTGGGAACCGGG
CAGTGCTGACATGCTCAGAACAAGATGGTTCCCCACCTTCTGAATACACCTGGTTCAAAGAT
GGGATAGTGATGCCTACGAATCCCAAAAGCACCCGTGCCCTTCAGCAACTCTTCCTATGTCTCT
GAATCCCACAACAGGAGAGCTGGTCTTTGATCCCCGTGCAGCCTCTGATACTGGAGAATACA
GCTGTGAGGCACGGAATGGGTATGGGACACCCATGACTTCAAATGCTGTGCGCATGGAAGCT
GTGGAGCGGAATGTGGGGGT CATCGTGGCAGCCGTCTTGTAAACCTGATTCTCTGGGAAT
CTTGGTTTTTGGCATCTGGTTTGCTATAGCCGAGGCCACTTTGACAGAACAAGAAAGGGA
CTTCGAGTAAGAAGGTGATTTACAGCCAGCCTAGTGCCCGAAGTGAAGGAGAATTCAAACAG
ACCTCGTCATTCTTGGTG TGA GCCTGGTCGGCTCACCGCCTATCATCTGCATTTGCCTTACT
CAGGTGCTACCGGACTCTGGCCCCCTGATGTCTGTAGTTTACAGGATGCCTTATTTGTCTTC
TACACCCACAGGGCCCCCTACTTCTTCGGATGTGTTTTTAATAATGTCAGCTATGTGCCCC
ATCCTCCTTCATGCCCTCCCTCCCTTTCCCTACCACTGCTGAGTGGCCTGGAAC TTGTTTAA
GTGTTTATTCCCCATTTCTTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCC
TTCTAAGTAGACAGCAAAAATGGCGGGGTGCGAGGAATCTGCACTCAACTGCCACCTGGC
TGGCAGGGATCTTTGAATAGGTATCTTGAGCTTGGTTCTGGGCTCTTTCCTTGTGTACTGAC
GACCAGGGCCAGCTGTTCTAGAGCGGAATTAGAGGCTAGAGCGGCTGAAATGGTTGTTGG
TGATGACACTGGGGTCCTTCCATCTCTGGGGCCACTCTCTTCTGTCTTCCCATGGGAAGTG
CCACTGGGATCCCTCTGCCCTGTCTCTCTGAATACAAGCTGACTGACATTGACTGTGTCTGT
GGAAAATGGGAGCTCTTGTGTGGAGAGCATAGTAAATTTTCAGAGAACTGAAGCCAAAAG
GATTTAAAACCGCTGCTCTAAAGAAAAGAAAAC TGGAGGCTGGGCGCAGTGGCTCACGCCTG
TAATCCCAGAGGCTGAGGCAGGCGGATCACCTGAGGTCGGGAGTTCCGGGATCAGCCTGACCA
ACATGGAGAAACCCTACTGGAAATACAAAGTTAGCCAGGCATGGTGGTGCATGCCTGTAGTC
CCAGCTGCTCAGGAGCCTGGCAACAAGAGCAAAACTCCAGCTCAAAAAAAAAAAAAAAAAA

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FIGURE 48

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSLAYSGFSSPRVEW
KFDQGDTRLVCYNNKITASYEDRVTFLLPTGITFKSVTREDTGTYYTCMVSEEGGNSYGEVKV
KLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPSEYTWFKDGIVMPTNPKSTRAFSNS
SYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTGMTSNAVRMEAVERNVGVIVA AVLVTLI
LLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGEFEKQTSSFLV

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 238-255

N-glycosylation site.

amino acids 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 270-274

Casein kinase II phosphorylation site.

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,
193-197, 203-207, 287-291

N-myristoylation site.

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

FIGURE 49

CCCACGCGTCCGAACCTCTCCAGCGATGGGAGCCGCCCGCCTGCTGCCCAACCTCACTCTGT
GCTTACAGCTGCTGATTCTCTGCTGTCAAACCTAGTACGTGAGGGACCAGGGCGCCATGACC
GACCAGCTGAGCAGGCGGCAGATCCGCGAGTACCAACTCTACAGCAGGACCAAGTTTGCCAAGCA
CGTGCAGGTACACGGGGCTCGCATCTCCGCCACCGCCGAGGACGGCAACAAGTTTGCCAAGC
TCATAGTGAGACGGACACGTTTGGCAGCCGGGTTTCGCATCAAAGGGGCTGAGAGTGAGAAG
TACATCTGTATGAACAAGAGGGGCAAGCTCATCGGGAAGCCCAGCGGGAAGAGCAAAGACTG
CGTGTTACGGAGATCGTGCTGGAGAACAACCTATACGGCCTTCCAGAACGCCCGGCACGAGG
GCTGGTTCATGGCCTTACGCGGCAGGGGCGGCCCGCCAGGCTTCCCGCAGCCGCCAGAAC
CAGCGCGAGGCCCACTTCATCAAGCGCCTCTACCAAGGCCAGCTGCCCTTCCCCAACCAACGC
CGAGAAGCAGAAGCAGTTCGAGTTTGTGGGCTCCGCCCCACCCGCCGGACCAAGCGCACAC
GGCGGCCCCAGCCCCCTACGTAGTCTGGGAGGCAGGGGGCAGCAGCCCTTGGGCCGCTCCC
CACCCCTTCCCTTCTTAATCCAAGGACTGGGCTGGGGTGGCGGGAGGGGAGCCAGATCCCC
GAGGGAGGACCCTGAGGGCCGGAAGCATCCGAGCCCCAGCTGGGAAGGGGCAGGCCGGTG
CCCCAGGGGCGGCTGGCACAGTGCCCCCTTCCCGACGGGTGGCAGGCCCTGGAGAGGAACT
GAGTGTACCCCTGATCTCAGGCCACCAGCCTCTGCCGGCCTCCAGCCGGGCTCCTGAAGCC
CGCTGAAAGGTCAGCGACTGAAGGCCTTGCAGACAACCGTCTGGAGGTGGCTGTCTCAAAA
TCTGCTTCTCGGATCTCCCTCAGTCTGCCCCCAGCCCCCAAACCTCCTCGCTAGACTGTA
GGAAGGGACTTTTGTGTTGTTGTTTGTTCAGGAAAAAGAAAGGGAGAGAGGAAAAATAG
AGGGTTGTCCACTCCTCACATTCCACGACCCAGGCCTGCACCCACCCCCAACTCCCAGCCC
CGGAATAAAACCATTTTCCTGC

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FIGURE 50

MGAARLLPNLTLCLQLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRISATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNRGKLIGKPSGKSKDCVFTEIVLENNYTAFQNNARHEGWFMATFRQGRPRQASRSRQNRQREAHFIKRLYQGQLFFPNHAEKQKQFEFVGSAPTRRTKRTRRPQPLT

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 9-13, 126-130

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 60-64

Casein kinase II phosphorylation site.

amino acids 65-69

Tyrosine kinase phosphorylation site.

amino acids 39-48, 89-97

N-myristoylation site.

amino acids 69-75, 188-194

Amidation site.

amino acids 58-62

HBGF/FGF family signature.

amino acids 103-128

FIGURE 51

GTGTGTCTCTCAGCAAAACAGTGGATTAAATCTCTTGCACAAGCTTGAGAGCAACACAA
TCTATCAGGAAAGAAAGAAAGAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAGA
AAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCAC
GGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCC
CCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGAGAGCGCCACCCTCAGGTGCACTATT
GACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGA
CAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCG
AGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAAC
CACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCAAAATTGTAGAGATTTCT
TTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGAC
CAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGAC
GAATACTTGGAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTC
CAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACCTATCCACCATACA
TTTCAGAAGCCAAGGTTACAGGTGTCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCC
TCAGCAGTCCCCTCAGCAGAATTCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAA
GAAAGGGGTGAAAGTGGAACAGACCTTTCCTCTCAAACTCATCTTCTTCAATGTCTCTG
AACATGACTATGGGAACTACACTTGGGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGC
ATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGCAACGGCACGTGAGGAGGGCAGG
CTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGACCTGCTTCTCAAATTTTTGATGTGAGTGCC
ACTTCCCCACCCGGGAAAGGCTGCCGCCACCACCACCAACACAACAGCAATGGCAACAC
CGACAGCAACCAATCAGATATATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGA
AATTTGAGGGAGGGGAACAAAGAATACTTTGGGGGAAAAGAGTTTAAAAAAGAAATTGAA
AATTGCCTTGAGATATTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGC
ACACCCGGCTTGACCCACTGCAAGCTGCATCGTGAACCTCTTTGGTGCCAGTGTGGGC
GGGCTCAGCCTCTCTGCCCACAGAGTGCCCCACGTGGAACATTCTGGAGCTGGCCATCCCCA
AATTCAATCAGTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGG
GCACCTTTGGTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAA
AAAAA

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FIGURE 52

MKTIQPKMHNSISWAIFTGLAALCLFQGVPRSGDATFPKAMDNVTVRQGESATLRCTIDNR
VTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTDNHPK
TSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFVSEDEYL
EIQGITREQSGDYECASNDVAAPVVRVKVTVNYPPYISEAKGTGVPVGQKGTQCEASAV
PSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNKLGHTNASIML
FGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLKLF

Signal peptide:

amino acids 1-28

[illegible]

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FIGURE 54

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59212

><subunit 1 of 1, 440 aa, 1 stop

><MW: 42208, pI: 6.36, NX(S/T): 1

MKFQGFLACLLLALCLSGEAGPLQSGEESTGTNIGEALGHGLGDALSEGVGKAIGKEAGGA
 AGSKVSEALGQGTREAVGTGVRQVPGFGAADALGNRVGEAAHALGNTGHEIGRQAEDVIRHG
 ADAVRGSWQGVPGHSGAWETSGGHGIFGSQGGGLGGQGQGNPGGLGTPWVHGYPGNSAGSFGM
 NPQGAPWGQGGNGGPPNFGTNTQGAVAPGYGSVRASNQNEGCTNPPPSGSGGGSSNSGGGS
 GSQSGSSGSGSNGDNNNGSSSGSSSGSSSGSSSGSSSGSSSGSSSGSGSGSRGDSGSESSW
 GSSTGSSSGNHGSGGGNGHKPGCEKPGNEARGSGESGIQGFRGQGVSSNMREISKEGNRLL
 GGSGDNRYRGQSSWGSGGGDAVGGVNTVNSETSPGMFNFDTFWKNFKSKLGFINWDAINKDQ
 RSSRIP

Signal peptide:

amino acids 1-21

N-glycosylation site.

amino acids 265-269

Glycosaminoglycan attachment site.

amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

Casein kinase II phosphorylation site.

amino acids 26-30, 109-113, 259-263, 300-304, 304-308

N-myristoylation site.

amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70,
 74-80, 90-96, 96-102, 130-136, 140-146, 149-155, 152-158,
 155-161, 159-165, 163-169, 178-184, 190-196, 194-200, 199-205,
 218-224, 236-242, 238-244, 239-245, 240-246, 245-251, 246-252,
 249-252, 253-259, 256-262, 266-272, 270-276, 271-277, 275-281,
 279-285, 283-289, 284-290, 287-293, 288-294, 291-297, 292-298,
 295-301, 298-304, 305-311, 311-317, 315-321, 319-325, 322-328,
 323-329, 325-331, 343-349, 354-360, 356-362, 374-380, 381-387,
 383-389, 387-393, 389-395, 395-401

Cell attachment sequence.

amino acids 301-304

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FIGURE 55

AGCCAGGCAGCACATCACAGCGGGAGGAGCTGTCCCAGGTGGCCCAGCTCAGCAATGGCAAT
GGGGGTCCCCAGAGTCATTCTGCTCTGCCTCTTTGGGGCTGCGCTCTGCCTGACAGGGTCCC
AAGCCCTGCAGTGCTACAGCTTTGAGCACACCTACTTTGGCCCCCTTTGACCTCAGGGCCATG
AAGCTGCCCAGCATCTCCTGTCTCATGAGTGCTTTGAGGCTATCCTGTCTCTGGACACCGG
GTATCGCGCGCCGGTGACCCTGGTGCGGAAGGGCTGCTGGACCGGGCCTCCTGCGGGCCAGA
CGCAATCGAACCCGGACGCGCTGCCGCCAGACTACTCGGTGGTGCGCGGCTGCACAACTGAC
AAATGCAACGCCCACCTCATGACTCATGACGCCCTCCCCAACCTGAGCCAAGCACCCGACCC
GCCGACGCTCAGCGGCGCCGAGTGCTACGCCTGTATCGGGGTCCACCAGGATGACTGCGCTA
TCGGCAGGTCCCAGAGTCCAGTGTCACCAGGACCAGACCGCCTGCTTCCAGGGCAGTGGC
AGAATGACAGTTGGCAATTTCTCAGTCCCTGTGTACATCAGAACCTGCCACCGGCCCTCCTG
CACCACCGAGGGCACCACCAGCCCCTGACAGCCATCGACCTCCAGGGCTCCTGCTGTGAGG
GGTACCTCTGCAACAGGAAATCCATGACCCAGCCCTTACCAGTGCTTCAGCCACCACCCT
CCCCGAGCACTACAGGTCTTGCCCTGCTCCTCCAGTCCTCCTGCTGGTGGGGCTCTCAGC
ATAGACCGCCCCCTCAGGATGCTGGGGACAGGGCTCACACACCTCATTCCTTGCTGCTTCAGC
CCCTATCACATAGCTCACTGGAAAATGATGTTAAAGTAAGAATTGCAAAA

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FIGURE 56

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA86576
><subunit 1 of 1, 251 aa, 1 stop
><MW: 26935, pI: 7.42, NX(S/T): 2
MAMGVPRVILLCLFGAALCLTGSQALQCYSFEHTYFGPFDLRAMKLPISCPHECFEAILSL
DTGYRAPVTLVRKGCWTGPPAGQTQSNPDALPPDYSVVRGCTTDKCNAHLMTHDALPNLSQA
PDPPTLSGAECYACIGVHQDDCAIGRSRRVQCHQDQTACFQGSGRMTVGNFSPVYIRTCNR
PSCTTEGTTSFWTAIDLQSGCEGYLCNRKSMTQPFTSASATTPPRALQVLALLLPVLLLVG
LSA

Important features of the protein:**Signal peptide:**

amino acids 1-19

Transmembrane domain:

amino acids 233-251

N-glycosylation sites.

amino acids 120-124, 174-178

N-myristoylation sites.

amino acids 15-21, 84-90

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FIGURE 57

GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCAGCCTCG
GCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCTGACTCCGTCCCGGCCAGGAGGGC
CATGATTTCCTCCCGGGGCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGGGGCTGA
GTGCCCTCGCGCCCCCTCGCGGGCCAGCTGCAACTGCACTTGCCCGCCAACCGGTTGCAG
GCGGTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGACGCGGGAGGTGTCTTC
ATCCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAGAAAAGGAGGATC
AGGTGTTGTCCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTATCCTTGGTCTACTCC
ATGCCCTCCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGAAAGACTCTGCCCCCTA
CAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGGCCACAGCATCAAAACCT
TAGAACTCAATGTACTGGTTTCCTCCAGCTCCTCCATCCTGCCGTCTCCAGGGTGTGCCCAT
GTGGGGGCAAACGTGACCTGAGCTGCCAGTCTCCAAGGAGTAAGCCCGCTGTCCAATACCA
GTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTTGCACCAGCATTAGATGTCAATCCGTG
GGTCTTTAAGCCTCACCAACCTTTCTGCTTCCATGGCTGGAGTCTATGTCTGCAAGGCCAC
AATGAGGTGGGCAC'TGCCCAATGTAATGTGACGCTGGAAGTGAGCACAGGGCCTGGAGCTGC
AGTGGTTGCTGGAGCTGTTGTGGGTACCCTGGTTGGACTGGGGTTGCTGGCTGGGCTGGTCC
TCTTGTAACACCGCCGGGGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCC
ATTGCTCCCCGACCCTGCCCTGGCCCAAGAGCTCAGACACAATCTCCAAGAATGGGACCCT
TTCCTCTGTACCTCCGCACGAGCCCTCCGGCCACCCCATGGCCCTCCCAGGCCCTGGTGCAT
TGACCCCCACGCCAGTCTCTCCAGCCAGGCCCTGCCCTC'ACCAAGACTGCCACGACAGAT
GGGGCCCACCCTCAACCAATATCCCCCATCCCTGGTGGGGTTTTCTTCTCTGGCTTGAGCCG
CATGGGTGCTGTGCCTGTGATGGTGCCTGCCAGAGTCAAGCTGGCTCTCTGGTAT**TGA**TGAC
CCCACCACTCATTGGCTAAAGGATTGGGGTCTCTCCTTCTATAAGGGTCACCTCTAGCAC
AGAGGCCTGAGTCATGGGAAAGAGTCACACTCCTGACCCCTTAGTACTCTGCCCCACCTCTC
TTTACTGTGGGAAAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGA
AGTGGATCTGGAATTGGGAGGAGCCTCCACCCACCCTGACTCCTCCTTATGAAGCCAGCTG
CTGAAATTAGCTACTACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCAGGC
CCCCTTGATCTGTACCCACCCCTATCTAACACCACCCTTGGCTCCCCTCCAGCTCCCTGT
ATTGATATAACCTGTGAGGCTGGCTTGGTTAGGTTTTACTGGGGCAGAGGATAGGGAATCTC
TTATTAATAACTAACATGAAATATGTGTTGTTTTTCATTTGCAAATTTAAATAAAGATACATAA
TGTTTTGTATGAAAAA

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FIGURE 58

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEVSS
SQPWEVFPVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKDSGPY
SCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSQCSPRSKPAVQYQ
WDRQLPSFQTFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLEVSTGPGAA
VVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWKSSDTISKNGTL
SSVTSARALRPFHGPPRPGALTPTPSLSSQALPSPRLPTTDGAHPQPISPIPGGVSSSGLSR
MGAVPVMVPAQSQAAGSLV

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 245-267

N-glycosylation site.

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

N-myristoylation site.amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,
262-268, 308-314, 363-369, 364-370**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 164-175

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FIGURE 59

ACTTGCCATCACCTGTTGCCAGTGTGGAAAAATTCGCCCTGTTGAATTTTTTGCACATGGAG
 GACAGCAGCAAAGAGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGAGATTATTTTAC
 CATACGCCCTCAGGACGTTCCCTCTAGCTGGAGTCTTGGACTTCAACAGAACCCCATCCAGT
 CATTTTGATTTTGCTGTTTATTTTTTTTTTCTTTTCTTTTCCACCACATTGTATTTTAT
 TTCCGTACTTTCAGAAATGAGGCCCTACAGACCACAAAGTGGCCCGACCCATGGGGCTTTTTTCC
 GAAGTCTTGGCTTATCATTTCCCTGGGGCTCTACTCACAGGTGTCAAACCTCCTGGCCTGCC
 CTAGTGTGTGCCGCTGCGACAGGAACCTTTGTCTACTGTAATGAGCGAAGCTTGACCTCAGTG
 CCTCTTGGGATCCCGGAGGGCGTAACCGTACTCTACCTCCACAACAACCAATTAATAATGC
 TGGATTTCCCTGCAGAACTGCACAAATGTACAGTCGGTGCACACGGTCTACCTGTATGGCAACC
 AACTGGACGAATTCCCATGAACCTTCCCAAGAATGTCAGAGTTCTCCATTTGCAGGAAAAC
 AATATTACAGACCATTTACGGGCTGCTCTTGCCAGCTCTTGAAGCTTGAAGAGCTGCACCT
 GGATGACAACCTCCATATCCACAGTGGGGGTGGAAGACGGGGCTTCCGGGAGGCTATTAGCC
 TCAAATGTTGTTTTGTCTAAGAATCACCTGAGCAGTGTGCCTGTTGGGCTTCTGTGGAC
 TTGCAAGAGCTGAGAGTGGATGAAAAATCGAATTGCTGTATATCCGACATGGCCTTCCAGAA
 TCTCACGAGCTTGGAGCGTCTTATTTGTGGACGGGAACCTCCTGACCAACAAGGGTATCGCCG
 AGGGCACCTTCAGCCATCTCACCAAGCTCAAGGAATTTCAATTGTACGTAATTCGCTGTCC
 CACCTCTCTCCGATCTCCCAGGTACGCATCTGATCAGGCTCTATTTGCAGGACAACAGAT
 AAACCAACATTCTTTGACAGCCTTCTCAAATCTGCGTAAGCTGGAACGGCTGGATATATCCA
 ACAACCAACTGCGGATGCTGACTCAAGGGGTTTTTGATAATCTCTCCAACCTGAAGCAGCTC
 ACTGCTCGGAATAACCTTGGTTTTGTGACTGCAGTATTAATGGGTACAGAAATGGCTCAA
 ATATATCCCTTCATCTCTCAACGTGCGGGGTTTTCATGTGCCAAGTCTTGAACAAGTCCGGG
 GGATGGCCGTGAGGGAATTAATATGAATCTTTTGTCTGTCCACCACGACCCCGGCCTG
 CCTCTCTTCACCCACAGCCCCAAGTACAGCTTCTCCGACCAETCAGCCTCCCACCTCTCTAT
 TCCAAACCTAGCAGAAGCTACAGCCTCCAACCTCCTACCACATCGAAACTTCCACGATTC
 CTGACTGGGATGGCAGAGAAAGAGTGACCCACCTATTTCTGAACGGATCCAGCTCTCTATC
 CATTTTGTGAATGATACTTCCATTCAAGTCAGCTGGCTCTCTCTCTTCCACCGTATGGCATA
 CAAACTCACATGGGTGAAAATGGGCCACAGTTTAGTAGGGGCATCGTTCAGGAGCGCATAG
 TCAGCGTGAGAAGCAACACCTGAGCCTGGTTAACTTAGAGCCCCGATCCACCTATCGGATT
 TGTTTTAGTGCCACTGGATGCTTTTAACTACCGCGCGGTAGAAGACACCATTGTTCAGAGGC
 CACCACCCATGCCTCTATCTGAACAACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGA
 CGTCCCAAGCATGGGCTCCCCCTTCTGCTGGCGGGCTTGATCGGGGGCGCGGTGATATTT
 GTGCTGGTGGTCTTGCTCAGCGTCTTTTGTGCTGGCATAATGCACAAAAAGGGGCGCTACACCTC
 CCAGAAGTGGAAATACAACCGGGGGCGGCGGAAAGATGATTATTGCGAGGCAGGCACCAAGA
 AGGACAACCTCCATCCTGGAGATGACAGAAACCAAGTTTCAGATCGTCTCCTTAAATAACGAT
 CAACTCCTTAAAGGAGATTTAGACTGCAGCCATTTACACCCCAATGGGGGCATTAATTA
 CACAGACTGCCATATCCCCAACATGCGATACTGCAACAGCAGCGTGCAGACCTGGAGC
 ACTGCCATACGTGACAGCCAGAGCCAGCGTTATCAAGCGGACAATTAGACTCTTGAGAA
 CACACTGTGTGTCACATAAAGACACGAGATTACATTTGATAAATGTTACACAGATGCAT
 TTGTGCATTTGAATACTCTGTAATTTATACGGTGTACTATATAATGGGATTTAAAAAAGTG
 CTATCTTTTCTATTTCAAGTTAATTACAAACAGTTTTGTAACCTTTTGCTTTTTAAATCTT

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FIGURE 60

MGLQTTKWPSHGAFFLKSWLIISLGLYSQVSKLLACPSVCRCDRNFVYCNERSLTSVPLGIP
EGVTVLYLHNNQINNAGFPAELHNVQSVHTVYLYGNQLDEFPMLPKNVRLHLQENNIQTI
SRAALAQLLKLEELHLLDINSISTVGVEDGAFREAI SKLLFLSKNHLSSVPVGLPVDLQELR
VDENRIAVISDMAFQNLTSLERLIVDGNLLTNKGIAEGTFSHLTKLKEFSIVRNSLSHPPPD
LPGTHLIRLYLQDNQINHIPLTAFSNLRKLERLDISNNQLRMLTQGVFDNLSNLKQLTARNN
PWFCDCSI KWVTEWLKYIPSSLNVRGFMCGPEQVRGMVRELMNLLSCPTTTPGLPLFTP
APSTASPTTQPPTLSIPNPSRSYTPPTTTSKLPTIPDWDGRERVTPPISERIQLSIHFVND
TSIQVSWLSLFTVMAYKLTWVKMGHSLVGGIVQERIVSGEKQHLSLVNLEPRSTYRICLVPL
DAFN YRAVEDTICSEATTHASYLNNGSNTASSHEQTTSHSMGSPFLLAGLIGGAVIFVLVVL
LSVFCWHMHKKGRYTSQKWYNRGRRKDDYCEAGTKKDNSILEMTETSQIVSLNNDQLLKG
DFRLQPIYTPNGGINYTDCHIPNNMRYCNSSVPDLEHCHT

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 542-561

N-glycosylation site.

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

Casein kinase II phosphorylation site.

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

Tyrosine kinase phosphorylation site.

amino acids 319-328

N-myristoylation site.amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,
522-528, 545-551, 633-639**Amidation site.**

amino acids 581-585

Leucine zipper pattern.

amino acids 164-186

Phospholipase A2 aspartic acid active site.

amino acids 39-50

FIGURE 61

TGAAGAGTAATAGTTGGAATCAAAAGAGTCAACGCAATGAAC TGTATTACTGCTGCGTTT
 TATGTTGGGAATTCCCTCCTATGGCCTTGTCTTGGAGCAACAGAAAAC TCTCAAACAAAGA
 AAGTCAAGCAGCCAGTGCATCTCATTTGAGAGTGAAGCGTGGCTGGGTGTGGAAACCAATTT
 TTTGTACCAGAGGAAATGAATACGACTAGTCATCACATCGGCAGCTAAGATCTGATTAGA
 CAATGGAAACAATTCTTTCCAGTACAGCTTTTGGGAGCTGGAGCTGGAAGTACTTTTATCA
 TTGATGAAAGAACAGGTGACATATATGCCATACAGAGCTTGATAGAGAGGAGCGATCCCTC
 TACATCTTAAGAGCCCAGGTAATAGACATCGCTACTGGAAGGGCTGTGGAACCTGAGTCTGA
 GTTTGTCTCAAAGTTTCGGATATCAATGACAATGAACCAAAATTCCTAGATGAACCTTATG
 AGGCCATTGTACCAGAGATGTCTCCAGAAGGAACATTAGTTATCCAGGTGACAGCAAGTGAT
 GCTGACGATCCCTCAAGTGGTAATAATGCTCGTCTCCTCTACAGCTTACTTCAAGGCCAGCC
 ATATTTTCTGTTTGAACCAACAGGAGTCATAAGAATATCTTCTAAATGGATAGAGAACA
 TGCAAGATGAGTATTGGGTAATCATTTCAAGCCAAGGACATGATTGGTCAGCCAGGAGCGTTG
 TCTGGAACAACAAGTGTTAATTAATAACTTTTTCAGATGTTAATGACAATAAGCCTATATTTAA
 AGAAAGTTTATACCGCTTGACTGTCTCTGAATCTGCACCCACTGGGACTTCTATAGGAACAA
 TCATGGCATATGATAATGACATAGGAGAGAATGCAGAAATGGATTACAGCATTGAAGAGGAT
 GATTTCGAAAACATTTGACATTATTACTAATCATGAACTCAAGAAGGAATAGTTATATTTAA
 AAAGAAAGTGGATTTTGTAGCACCAGAACCACTACGGTATTAGAGCAAAAAGTTAAAAACCATC
 ATGTTCCCTGAGCAGCTCATGAAGTACCACACTGAGGCTTCCACCCTTTTATTAAAGATCCAG
 GTGGAAGATGTTGATGAGCCTCCTCTTTTCTCCTTCCATATTATGTTTGAAGTTTGTGA
 AGAAACCCACAGGGATCATTTGTAGGCGTGGTGTCTGCCACAGACCCAGACAATAGGAAAT
 CTCCTATCAGGTATTCTATTACTAGGAGCAAGTGTTTCAATATCAATGATAATGGTACAATC
 ACTACAAGTAACTCACTGGATCGTGAATCAGTGTCTGGTACAACCTAAGTATTACAGCCAC
 AGAAAAATACAAATAGAACAGATCTCTTCGATCCCCTGTATGTGCAAGTCTTCTAACATCA
 ATGATCATGCTCCTGAGTCTCTCAATACTATGAGACTTATGTTTGTGAAATGAGGCTCT
 GGTCAAGTAATTCAGACTATCAGTGCAGTGGATAGAGATGAATCCATAGAAGAGCACCATT
 TTACTTTAATCTATCTGTAGAAGACACTACAATTCAGTTTACAAATCATAGATAATCAAG
 ATAACACAGCTGTCAATTTGACTAATAGAACTGGTTTAACTTCAAGAAGAACCTGTCTTC
 TACATCTCCATCTTAATTGCCGACAATGGAAATCCCGTCACTTACAAGTACAAACACCCTTAC
 CATCCATGTCTGTGACTGTGGTGACAGTGGGAGCACACAGACCTGCCAGTACCAGGAGCTTG
 TGCTTTCCATGGGATTCAAGACAGAAGTTATCATTGCTATTCTCATTTGCTATGATCATATA
 TTTGGGTTTATTTTTTGTACTTTGGGTTTAAAAACAACGGAGAAAACAGATTCTATTTCTCTGA
 GAAAAGTGAAGATTTTCAAGAGAGAATATATTTCCAATATGATGATGAAGGGGGTGGAGAAGAAG
 ATACAGAGGCCCTTTGATATAGCAGAGCTGAGGAGTAGTACCATAATGCGGGAACGCAAGACT
 CGGAAAACCCACAAGCGCTGAGATCAGGAGCCTATACAGGCAAGTCTTGTGCAAGTTGGCCCGA
 CAGTGGCCATATTCAGGAAATTCATTCTGGAAAAGCTCGAAGAAGCTAATACTGATCCGTGTG
 CCCTCCTTTTTGATTCCCTCCAGACCTACGCTTTTGGGGAACAGGGTCATTAGCTGGATCC
 CTGAGCTCCTTTAGAAATCAGCATCTCTGATCAGGATGAAGCTTATGATTCTTAAATGAGTT
 GGGACCTCGCTTTAAAAAGATTAGCATGCATGTTTGGTCTGCAAGTGCAGTCAAAATATTAGG
 GCTTTTACCATCAAAATTTTTTAAAGTGCTAATGTGTATTGCAACCCATGGTAGTCTTAA
 AGAGTTTGTGCCCCGGCTCTATGGCGGGGAAAGCCCTAGTCTATGGAGTTTCTGATTCTCC
 CTGGAGTAAATACCTCCATGGTTATTTTAAAGTACCTACATGCTGTGATTGAACAGAGATGTG
 GGGAGAAATGTAAACAATCAGCTCACAGGCATCAATACAACCAGATTTGAAGTAAATATATG
 TAGGAAGATATTAAGTAGATGAGAGGACACAAGATGTAGTCGATCCTTATGCGATTATAT
 CATTTATTACTTAGGAAAGAGTAAAAATACCAACGAGAAAAATTAAGGAGCAAAAAATTTG
 CAAGTCAAAATAGAAATGTACAAATCGAGATAACATTACATTTCTATCATATTGACATGAAA
 ATTGAAAATGTATAGTCAGGAAATTTTCATGAATTATCCATGAAGTATGTTTCTCTTAT
 TTAAA

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FIGURE 63

CTTCAGAACAGGTTCTCCTTCCCCAGTCACCAGTTGCTCGAGTTAGAATTGTCTGCAATGGC
CGCCCTGCAGAAATCTGTGAGCTCTTTCCTTATGGGGACCCTGGCCACCAGCTGCCTCCTTC
TCTTGGCCCTCTTGGTACAGGGAGGAGCAGCTGCGCCCATCAGCTCCCAGTGCAGGCTTGAC
AAGTCCAACCTCCAGCAGCCCTATATCACCAACCGCACCTTCATGCTGGCTAAGGAGGCTAG
CTTGGCTGATAACAACACAGACGTTTCGTCTCATTGGGGAGAACTGTTCCACGGAGTCAGTA
TGAGTGAGCGCTGCTATCTGATGAAGCAGGTGCTGAACTTCACCCTTGAAGAAGTGTGTTC
CCTCAATCTGATAGGTTCCAGCCTTATATGCAGGAGGTGGTGCCTTCCTGGCCAGGCTCAG
CAACAGGCTAAGCACATGTCATATTGAAGGTGATGACCTGCATATCCAGAGGAATGTGCAAA
AGCTGAAGGACACAGTGAAAAAGCTTGGAGAGAGTGGAGAGATCAAAGCAATTGGAGAAGTG
GATTTGCTGTTTTATGTCTCTGAGAAATGCCTGCATTTGACCAGAGCAAAGCTGAAAAATGAA
TAACTAACCCCTTTCCTGCTAGAAATAACAATTAGATGCCCCAAAGCGATTTTTTTTAAAC
CAAAAGGAAGATGGGAAGCCAAACTCCATCATGATGGGTGGATTCCAAATGAACCCCTGCGT
TAGTTACAAAGGAAACCAATGCCACTTTTGTTTATAAGACCAGAAGGTAGACTTCTAAGCA
TAGATATTTATTGATAACATTTTCATTGTAAGTGGTGTCTATACACAGAAAACAATTTATTT
TTTAAATAATTGTCTTTTCCATAAAAAAGATTACTTTCATTTCCTTTAGGGGAAAAAACCC
CTAAATAGCTTCATGTTTCCATAATCAGTACTTTATATTTATAAATGTATTTATTATTATTA
TAAGACTGCATTTTATTTATATCATTTTATTAATATGGATTTATTTATAGAAACATCATTCG
ATATTGCTACTTGAGTGTAAGGCTAATATTGATATTTATGACAATAATTATAGAGCTATAAC
ATGTTTATTTGACCTCAATAAACACTTGATATCCC

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FIGURE 64

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA125185
><subunit 1 of 1, 179 aa, 1 stop
><MW: 20011, pI: 8.10, NX(S/T): 3
MAALQKSVSSFLMGTLATSCLLLLALLVQGGAAPISSHCRLDKSNFQQPYITNRTFMLAKE
ASLADNNTDVRLLIGEKLFGVSMSERCYLMKQVLNFTLEEVLPQSDRFQPYMQEVVPFLAR
LSNRLSTCHIEGDDDLHIQRNVQKLKDTVKKLGESGEIKAIGELDLLFMSLRNACI

Important features of the protein:**Signal peptide:**

amino acids 1-33

N-glycosylation sites.

amino acids 54-58, 68-72, 97-101

N-myristoylation sites.

amino acids 14-20, 82-88

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 10-21

FIGURE 65

GCCCTAACCTTCCCAGGGCTCAGCTCTTTGGAGCTGCCCATTCCTCCGGCTGCGAGAAAGGA
 CGCGCGCCCTGCGTCGGGGCGAAGAAAAGAAGCAAACTTGTCCGGGAGGGTTTCGTCATCAAC
 CTCCTTCCCGCAAACCTAAACCTCCTGCCGGGGCCATCCCTAGACAGAGGAAAAGTTCTCTGCA
 GAGCCGACCGAGCCCTAGTGGATCTGGGGCAGGCAGCGCGCTGGTGTGGAATTAGATCTGT
 TTTGAACCCAGTGGAGCGCATCGCTGGGGCTCGGAAGTCACCGTCCGCGGGCACC GG GTTGG
 CGCTGCCCGAGTGGAACCGACAGTTTGCAGCCTCGGCTGCAAGTGGCCTCTCCTCCCCGCG
 GTTGTGTTCAGTGTCCGGTGAGGGCTGCGAGTGTGGCAAGTTGCAAGAGAGCCCTCAGAGG
 TCCGAAGAGCGCTGCGCTCCTACTCGCGTTTCGCTTCTTCTCCTCTTCGGTTCCCTACTGTGA
 AATCGCAGCGACATTTACAAAGGCCCTCCGGGTCTTACCGAGACCGATCCGCAGCGTTTGGCC
 CGGTCTGCCTATTGCATCGGGAGCCCCGAGCACCGGCGAAATGCGCGAGGTTCCCGAAGGC
 CGACCTGGCCGCTGCAGGAGTTATGTTACTTTGCCACTTCTTCACGGACAGTTTCAGTTTCG
 CCGATGGGAAACCCGGAGACCAAATCCTTGATTGGCAGTATGGAGTTACTCAGGCCTTCCCT
 CACACAGAGGAGGAGGTGGAAGTTGATTACACGCGCTACAGCCACAGGTGGAAGAAAAGAACTT
 GGACTTCTCAAGGCGGTAGACACGAACCGAGCAAGCGTCCGGCAAGACTCTCCTGAGCCCA
 GAAGCTTCACAGACCTGCTGCTGGATGATGGGCAGGACAATAACACTCAGATCGAGGAGGAT
 ACAGACCACAATTACTATATATCTCGAATATATGGTCCATCTGATTTCTGCCAGCCGGGATTT
 ATGGGTGAACATAGACCAAATGGAAGAGATAAAGTGAAGATTTCATGGAATATTGTCCAATA
 CTCATCGGCAAGCTGCAAGAGTGAATCTGTCCTTCGATTTTCCATTTTATGGCCACTTCCCTA
 CGTGAAATCACTGTGGCAACCGGGGGTTTCATATACACTGGAGAAGTCGTACATCGAATGCT
 AACAGCCACACAGTACATAGCACCTTTAATGGCAAATTTTCGATCCCACTGTATCCAGAAATT
 CAAGTGTGAGATATTTTGATAATGGCACAGCACTTGTGGTCCAGTGGGACCATGTACATCTC
 CAGGATAATTATAACCTGGGAAGCTTCACATTCCAGGCAACCTGCTCATGGATGGACGAAT
 CATCTTTGGATACAAAGAAATTCCTGTCTTGGTCACACAGATAAGTTCAACCAATCATCCAG
 TGAAGTCGGACTGTCCGATGCATTTGTGCTTGTCCACAGGATCCAAACAAATTCCTCAATGTT
 CGAAGAAGAACAATTTATGAATACCACCGAGTAGAGTACAAATGTCAAAATTTACCAACAT
 TTCGGCTGTGGAGATGACCCCATTAACCATGCTCCAGTTTAAACAGATGTGGCCCTGTG
 TATCTTCTCAGATTGGCTTCAACTGCAGTTGGTGTAGTAAACTTCAAAGATGTTCCAGTGGA
 TTTGATCGTCATCGGCAGGACTGGGTGGACAGTGGATGCCCTGAAGAGTCAAAAGAGAAGAT
 GTGTGAGAAATACAGAACCAGTGGAACTTCTTCTCGAACCACCACAACCGTAGGAGCGCAAC
 CCACCCAGTTCAGGGTCTTAACCTACCACCAGAAGAGCAGTGAAGTTCTAGTTTCCCAACGAGC
 CTCCTACAGAAGATGATACCAAGATAGCACTACATCTAAAGATATATGGAGCTTCTACAGA
 TGACAGTGCAGCTGAGAAGAAAGGGGGAACCTCCACGCTGGCCTCATATTGGAATCCTCA
 TCCTGGTCTCTATTGTAGCCACAGCCATTCTTGTGACAGTCTATATGTATCACCACCCAACA
 TCAGCAGCCAGCATCTTCTTTATTGAGAGACGCCCAAGCAGATGGCCTGCCATGAAGTTAG
 AAGAGGCTCTGGACATCCTGCCTATGCTGAAGTTGAACCAAGTTGGAGAGAAAGAAGGCTTTA
 TTGTATCAGAGCAGTGCATAAATTTCTAGGACAGAACACACCAAGTACTGGTTTTACAGGTGT
 TAAGACTAAAATTTTGCTATACCTTTAAGACAAACAAACACACACACAAACAAAGCTC
 TAAGCTGCTGTAGCCTGAAGAAGACAAGATTTCTGGACAAGCTCAGCCAGGAAACAAAGGG
 TAAACAAAAAACTAAAACCTATACAAGATACCATTTACACTGAACATAGAATTCCCTAGTGG
 AATGTCATCTATAGTTCACTCGGAACATCTCCCGTGGACTTATCTGAAGTATGACAAGATTA
 TAATGCTTTTGGCTTAGTGTCAGGGTTGCAAGGGATCAGAAAAAAAATCATATAAAGC
 TTTAGTTCATGAGGG

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FIGURE 66

MARFPKADLAAAGVMLLCHFFTDQFQFADGKPGDQILDWQYGVTVQAFPHTEEEVEVD SHAYS
 HRWKRNLDLFLKAVDTNRASVGQDSPEPRSFTDLLDDGQDNNQTIEEDTDHNYISRIYGPS
 DSASRDLWVNIDQMEKDKVKIHGILSNTHRQAARVNLSFDFPFYGHFLREITVATGGFIYTG
 EVVHRMLTATQYIAPLMANFDPVSRNSTVRYFDNGTALVVQWDHVHLQDNYNLGSFTFQAT
 LLMDGRIIFGYKEIPVLVTQISSTNHPVKVGLSDAFVVVHRIQQIPNVRRRTIYEHVELQ
 MSKITNISAVEMTLPPTCLQFNRCGPCVSSQIGFNCSWCSKLQRCSSGFDRHRQDWVDSGCP
 EESKEKMCENTEPVETSSRTTTTVGATTTQFRVLTTTTRAVTSQFPTSLPTEDDTKIALHLK
 DNGASTDDSAAEKGGTLHAGLIIGILILVLIVATAILVTVMYHHPTSAASIFFIERRPSR
 WPAMKFRRGSGHPAYAEVEFPVGEKEGFIVSEQC

Important features of the protein:**Transmembrane domain:**

amino acids 454-478

N-glycosylation sites.

amino acids 103-107, 160-164, 213-217, 221-225, 316-320, 345-349

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 297-301, 492-496, 503-507

N-myristoylation sites.amino acids 42-48, 100-106, 147-153, 279-285, 397-403, 450-456,
455-461

FIGURE 67A

GCAGCCCTAGCAGGGATGACATGATGCTGTTGGTGCAGGGTGCTTGTGCTCGAACCAAGTG
GCTGGCGGCGGTGCTCCTCAGCCTGTGCTGCCTGCTACCCTCCTGCCTCCCGGCTGGACAGA
GTGTGGACTTCCCCTGGGCGGCCGTGGACAACATGATGGTCAGAAAAGGGACACGGCGGTG
CTTAGGTGTTATTTGGAGATGGAGCTTCAAAGGGTCTGCTGGCTGAACCGGTCAAGTATTAT
TTTTGCGGGAGGTGATAAGTGGTCAGTGGATCCTCGAGTTTCAATTTCAACATTGAATAAAA
GGGACTACAGCCTCCAGATACAGAATGTAGATGTGACAGATGATGGCCATACACGTGTTCT
GTTCAGACTCAACATACACCCAGAACAATGCAGGTGCATCTAACTGTGCAAGTTCCTCCTAA
GATATATGACATCTCAAATGATATGACCGTCAATGAAGGAACCAACGTCACTCTTACTTGTT
TGGCCACTGGGAAACCAGAGCCTTCCATTTCTTGGCGACACATCTCCCATCAGCAAAACCA
TTTGAAAATGGACAATATTTGGACATTTATGGAATTACAAGGGACCAGGCTGGGGAATATGA
ATGCAGTGCAGAAAATGATGTGTCATTTCCAGATGTGAGGAAAGTAAAAGTTGTTTCAACT
TTGCTCCTACTATTTCAGGAAATTAATCTGGCACCGTGACCCCCGGACGCAGTGGCCTGATA
AGATGTGAAGGTGCAGGTGTGCCGCCCTCCAGCCTTTGAATGGTCAAAAGGAGAGAAGAAGCT
CTTCAATGGCCAACAAGGAATTATTATCAAATTTAGCACAAAGTCCATTCTCACTGTTA
CCAACGTGACACAGGAGCACTTCGGCAATTATACTTGTGTGGCTGCCAACAAGCTAGGCACA
CCATGCGAGCCTGCCCTCTTAACCCCTCAAGTACAGCCAGTATGGAATTACCGGGAGCGC
TGATGTTCTTTCTCCTGCTGGTACCTTGTGTTGACATGTCTCTTTACCAGCATATTCT
ACCTGAAGAATGCCATTTACAATAAATTCAGAGCCATAAAAGGCTTTTAAGGATCTCTCT
GAAAGTGCTGATGGCTGGATCCAATCTGGTACAGTTTGTAAAAGCAGCGTGGGATATAATC
AGCAGTGCTTACATGGGGATGATCGCCTTCTGTAGAAATTGCTCATTATGTAATACTTTAAT
TCTACTCTTTTGGATTGCTACATTACCTTGTGAAGCAGTACACATTTGCGCTTTTAAAG
ACGTGAAAGCTCTGAAATTACTTTTAGAGGATATTAATTGTGATTTTCATGTTTGTAACTAC
AACTTTTCAAAGCATTTCAGTCAATGCTGCTAGGTTGACAGGCTGTAGTTTACAAAAACGAA
TATTGCACTGAAATATGATCTTTTAAAGGCTGCAATTAAGCAGTTCAGTTCCCTGTTTCAAT
AAGAGTCAATCCACATTTACAAGATGCATTTTTTCTTTTTTGATAAAAAAGCAAATAATA
TTGCCTTCAGATATTTTCTCAAATATAACACATATCTAGATTTTCTGCTCGCATGATAT
TCAGGTTTCAGGAATGAGCCTTGTAATATAACTGGCTGTGCGAGCTTGGCTCTCTTCTCTGT
AAGTTCAGCATGGGTGTGCCTTCATACAATAATATTTTTCTCTTTGTCTCCAACATAATAA
AATGTTTTGCTAAATCTTACAATTTGAAAGTAAAAATAAACAGAGTGATCAAGTTAAACCA
TACATATCTCTAAGTAACGAAGGAGCTATTGGACTGTAAAGTCTCTTCTGCACTGACAA
TGGGGTTTGAGAATTTTGCCCCACACTAACTCAGTTCTTGTGATGAGAGACAAATTAATAAC
AGTATAGTAAATATACCATATGATTTCTTTAGTTGTAGCTAAATGTTAGATCCACCGTGGGA
AATCATATCCCTTTAAAATGACAGCACAGTCCACTCAAAGGATTGCCCTAGCAATACAGCATCT
TTTTCTTTCACTAGTGCAGCCAAAAATTTTAAGATGATTTGTCAAGAAAGGACCAAGTCC
TATCACCTAATATTACAAGAGTTGGTAAGCGCTCATCATTAATTTTATTTTGTGGCAGCTAA
GTTAGTATGACAGAGGCGAGTGTCTCCTGTGGACAGGAGCATTTTGCATATTTTCCATCTGAAA
GTATCATCAGTTGATGCTTGGAAATGCATGTTATATATTTTAAACTTCCAAAAATATTATA
TAACAAACATTCTATATCGGTATGTAGCAGACCAATCTCTAAAATAGCTAATTCTTCAATAA
AATCTTTCTATATGCAATTTTCAGTGCAAAACAGTAAAGTCAAAAAGACCATCTTTTATTT
TTCTTTACATGATATATGTAAGATGCGATCAAATAAAGACAAAACCAAGTATGAGAATAT
CTTAAGATAAGTAATTATCAAATTATTGTGAATGTTAAATTAATTTCTACTATAAAGGAAGCAA
AACTACATTTTGAAGGAAAATGCTGTACTCTAACATTAATTTACAGGAATAGTTTGATGG
TTTCACTCTTTACTAAAGAAAGGCCATCACCTTGAAGGCCATTTTACAGGTTTGTATGAAGTT
ACCAATTTTCAGTACACCTAAATTTCTACAAATAGTCCCTTTTACAGGTGTAACAAACAAAG
ACCCTATAATAAAATTAGATACAAGAAATTTTGCAGTGGTTATACATATTTGAGATATCTAG
TATGTTGCCCTAGCAGGGATGGCTTAAAAACTGTGATTTTTTTTCTCAAGTAAACATTAGT
CCCAAGTACATCATATAAATTTTAAATAGAAAAATGAATCTTAAATGAGGGGACATAAG
TATACTCTTTCCACAAAATGGCAATAATAAGGCATAAAGCTAGTAAATCTACTAACTGTAAT
AAATGTATGACATTAATTTTGTATGATACATTAATAAAGAGTTTTTTGAACAAATATGGCATT
TAACTTTATTTATTTTGTCTTTTAAAGAAATATTTTGTGGAATTTGTGAATAACTATAA
AATATTATTTTGTATTGCGACCTTTAAAGTGGCACACTCCATAAATATCTACTTAGAAAT

FIGURE 67B

AGTGGTGCTACCACAAAAAATGTTAACCATCAGTACCATTGTTTGGGAGAAAGAAACAGATC
AAGAATGCATATTATTACAGTGACCGCTTTCCTAGAGTTAAAATACCTCCTCTTTGTAAGGTT
TGTAAGGTAAATTGAGGTATAAACTATGGATGAACCAAATAATTAGTTCAAAGTGTTGTCATG
ATTCCAAATTTGTGGAGTCTGGTGTTTTTACCATAGAATGTGACAGAAGTACAGTCATAGCT
CAGTAGCTATATGTATTTGCCTTTATGTTAGAAGAGACTTTCTTGAGTGACATTTTTAAATA
GAGGAGGTATTCACATATGTTTTTCTGTATCACAGCAGCATTCCTAGTCCTTAGGCCCTCGGA
CAGAGTGAAATCATGAGTATTTATGAGTTCATATTTGTCAAATAAGGCTACAGTATTTGCTT
TTTTGTGTGAATGTATTGCATATAATGTTCAAGTAGATGATTTTACATTTATGGACATATAA
AATGTCTGATTACCCCATTTTATCAGTCCTGACTGTACAAGATTGTTGCAATTCAGAATAG
CAGTTTTATAAATTGATTTATCTTTTAACTATAACAATTTGTGTTAGCTGTTTCATTTCCAGG
ANTATATTTTCTACAAGTTCACCTTGTTGGGACTCCTTTTGTTGCCCTATTTTTTTTTAAAG
AAGGAAGAAAGAAAAAATAAGTAGCAGTTTAAAAATGAGAATGGAGAGAAAAGAAAAGAATG
AAAAGGAAAGGCAGTAAAGAGGGAAAAAAAAGGAAGGATGGAAGGAATGAAGGAAGGAAGGG
AGGAAGGGGAGAAGGTAGGAAGAAAGAAAGGATGAGAGGGAAGGAAGAATCAGAGTATTAGG
GTAGTTAACTTACACATTTGCATTCTTAGTTTAACTGCAAGTGGTGTAAGTATGTTTTTCAA
TGATCGCATTTGAAACATAAGTCCTATTATACCATTAAAGTTCCATTATGCAGCAATTATAT
AATAAAAAGTACTGCCCAAGTTATAGTAATGTGGGTGTTTTTGAGACACTAAAAGATTTGAG
AGGGAGAATTTCAAACCTTAAAGCCACTTTTGGGGGGTTTATAACTTAACTGAAAAATTAATG
CTTCATCATAACATTTAAGCTATATCTAGAAAGTAGACTGGAGAACTGAGAAAAATTACCCAG
GTAATTCAGGGAAAAAAAATATATATATATATAAATACCCCTACATTTGAAGTCAGAAA
ACTCTGAAAAACTGAATTATCAAAGTCAATCATCTATAATGATCAAATTTACTGAACAATTG
TTAATTTATCCATTGTGCTTAGCTTTGTGACACAGCCAAAAGTTACCTATTTAATCTTTTCA
ATAAAAATTGTTTTTTGAAATCCAGAAATGATTTAAAAAGAGGTCAGGTTTTTAACTATTTA
TTGAAGTATGTGGATGTACAGTATTTCAATAGATATGAATATGAATAAATGGTATGCCTTAA
GATTCTTTGAATATGTATTTACTTTAAAGACTGAAAAAGCTCTTCCTGTCTTTTAGTAAAA
CATCCATATTTCATAACCTGATGTAAAAATATGTTGTAAGTGTTCCTAATAGGTGAATATAAAC
TCAGTTTATCAATTAATAA

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FIGURE 68

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA92259

><subunit 1 of 1, 354 aa, 1 stop

><MW: 38719, pI: 6.12, NX(S/T): 6

MDMMLLVQGACCSNQWLA AVL LSLCCLLPSCLPAGQSVDFPWA AVDNMMVRKGD TAVLRCYL
EDGASKGAWLNRSSII FAGGDKWSVDPRVSISTLNKRDSLQIQNV DVTDDGPYTCSVQTQH
TPRTMQVHLTVQVPPKIYDISNDMTVNEGTVTLTCLATGKPEPSISWRHISPSAKPFENGQ
YLDIYGITRDQAGEYEC SAENDVSFPDVRKVKVVVNFAPTIQEIKSGTVTPGRSGLIRCEGA
GVPPPAFEWYKGEKKLFNGQQGII IQNFSTRSILTVTNVTQEHFGNYTCVAANKLGTNASL
PLNPPSTAQYGITGSADVL FSCWYLVLTLSSTSFIFYLKNAILQ

Important features of the protein:**Signal peptide:**

amino acids 1-33

Transmembrane domain:

amino acids 322-343

N-glycosylation sites.

amino acids 73-77, 155-159, 275-279, 286-290, 294-298, 307-311

Tyrosine kinase phosphorylation site.

amino acids 180-188

N-myristoylation sites.amino acids 9-15, 65-71, 69-75, 153-159, 241-247, 293-299,
304-310, 321-327**Myelin P0 protein.**

amino acids 94-123

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FIGURE 69

ATAGTAGAAGAATGTCTCTGAAATTACTGGATGAGTTTCAGTCATACTTTACATGGGCACA
ATTTACATTCAAGCTCCTTATCCTAGGCTAATTTTATATTATGTTAAATCACTTGTTTTG
TTCTCACGGCTTCCTGCCTGCTATAGGCATAATTACGAGGAAGCAGAACTTCTCCAGAAGCA
AGCGCACATGCGTTCCAAAATAAGAGCAAATTCGCTCTAAACACAGGAAAAGACCTGAAGCT
TTAATTAAGGGGTACATCCAACCCAGAGCGCTTTTGTGGGCACTGATTGCTCCAGCTTCT
GCGTCACTGCGCGAGGGAAGAGGGAAGAGGATCCAGGCGTTAGACATGTATAGACACAAAA
CAGCTGGAGATTGGGCTTAAAATACCCACCAAGCTCCAAAGAAGAGACCCAAGTCCCCAAA
CATTGATTTCAAGGGTGCCAGGAAGGAAGAGCAGCAGCAGGGTGGGAGAGAAGCTCCAGTCA
GCCACAAGATGCCATTGTCCCCGGCCTCCTGCTGCTGCTGCTCTCCGGGGCCACGGCCAC
CGCTGCCCTGCCCTGGAGGGTGGCCCCACCGGCCGAGACAGCGAGCATATGCAGGAAGCGG
CAGGAATAAGGAAAAGCAGCCTCCTGACTTTCCTCGCTTGGTGGTTTGAGTGGACCTCCAG
GCCAGTGCCGGGCCCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGCGGCAGGAAGGCGC
ACCCCCCAGCAATCCGCGCGCCGGGACAGAATGCCCTGCAGGAACCTCTTCTGGAAGACCT
TCTCCTCCTGCAAATAG

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FIGURE 70

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA44175
><subunit 1 of 1, 155 aa, 1 stop
><MW: 17194, pI: 10.44, NX(S/T): 0
MYRHKNSWRLGLKYPPSSKEETQVPKTLISGLPGRKSSSRVGEKLQSAHKMPLSPGLLLLLL
SGATATAALPLEGGPTGRDSEHMQEAGIRKSSLLTFLAWWFEWTSQASAGPLIGEEAREVA
RRQEGAPPQQSARRDRMPCRNFFWKTFSSCK

Important features of the protein:**Transmembrane domain:**

amino acids 51-69

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 35-39, 92-96

N-myristoylation sites.

amino acids 64-70, 75-81, 90-96

Amidation site.

amino acids 33-37

72/75

FIGURE 71

GTCGTGTGCTTGGAGGAAGCCGCGGAACCCCCAGCGTCCGTCCTCCATGGCGGTGGAGCCTTGGGA
GCTGGCTGGGTGGCTGCCTGCTGGTGTGTCAGCATTTGGGAATGGTACCACCTCCCGAAAATGTC
AGAATGAATTCTGTTAATTTCAAGAACATTCTACAGTGGGAGTCACCTGCTTTTGCCAAAGG
GAACCTGACTTTCACAGCTCAGTACCTAAGTTATAGGATATTCCAAGATAAATGCATGAATA
CTACCTTGACGGAATGTGATTTCTCAAGTCTTTCCAAGTATGGTGACCACACCTTGAGAGTC
AGGGCTGAATTTGCAGATGAGCATTGAGACTGGGTAAACATCACCTTCTGTCTGTGGATGA
CACCATTATTGGACCCCTGGAATGCAAGTAGAAGTACTTGCTGATTCTTTACATATGCGTT
TCTTAGCCCCATAAATTGAGAATGAATACGAAACTTGGACTATGAAGAATGTGTATAACTCA
TGGACTTATAATGTGCAATACTGGAAAAACGGTACTGATGAAAAGTTTCAAATTACTCCCCA
GTATGACTTTGAGGTCCCTCAGAAACCTGGAGCCATGGACAACCTATTGTGTTCAGTTTCGAG
GGTTTCTTCTCTGATCGGAACAAAGCTGGGGAATGGAGTGAGCCTGTCTGTGAGCAAAACAACC
CATGACGAAACGGTCCCCCTCCTGGATGGTGGCCGTATCCTCATGGCTCGGTCTTCATGGT
CTGCCTGGCACTCCTCGGCTGCTTCTCCTTGCTGTGGTGCCTTTACAAGAAGACAAAGTACG
CCTTCTCCCTAGGAATTCTCTTCCACAGCACCTGAAAGAGTTTTTGGGCCATCCTCATCAT
AACACACTTCTGTTTTTCTCCTTTCCATTGTCGGATGAGAATGATGTTTTTGACAAGCTAAG
TGTCATTGCAGAAGACTCTGAGAGCGGCAAGCAGAATCCTGGTGACAGCTGCAGCCTCGGGA
CCCCGCCTGGGCAGGGGCCCAAAGCTTAGGCTCTGAGAAGGAAACACACTCGGCTGGGCACA
GTGACGTACTCCATCTCACATCTGCCTCAGTGAGGGATCAGGGCAGCAAACAAGGCCAAGA
CCATCTGAGCCAGCCCCACATCTAGAACTCCAGACCTGGACTTAGCCACCAGAGAGCTACAT
TTTAAAGGCTGTCTTGCGAAAAATACTCCATTTGGGAACTCACTGCCTTATAAAGGCTTTCA
TGATGTTTTTCAGAAGTTGGCCACTGAGAGTGTAATTTTCAGCCTTTTATATCACTAAAATAA
GATCATGTTTTAATTGTGAGAAACAGGGCCGAGCACAGTGGCTCACGCCTGTAATACCAGCA
CCTTAGAGGTCGAGGCAGGCGGATCACTTGAGGTGAGGAGTTCAAGACCAGCCTGGCCAATA
TGGTGAAACCCAGTCTCTACTAAAAATACAAAAATTAGCTAGGCATGATGGCGCATGCCAT
AATCCCAGCTACTCGAGTGCCTGAGGCAGGAGAATTGCATGAACCCGGGAGGAGGAGGAGGA
GGTTGCAGTGAGCCGAGATAGCGGCACTGCACTCCAGCCTGGGTGACAAAGTGAGACTCCAT
CTCAAAAAAAAAAAAAAAAAAATTGTGAGAAACAGAAATACTTAAATGAGGAATAAGAATGG
AGATGTTACATCTGGTAGATGTAACATTCTACCAGATTATGGATGGACTGATCTGAAAATCG
ACCTCAACTCAAGGGTGGTCAGCTCAATGCTACACAGAGCACGGACTTTTGGAATCTTTGCA
GTACTTTGAATTTATTTTCTACCTATATATGTTTTATATGCTGCTGGTGTCTCCATTAAAGT
TTTACTCTGTGTTGC

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FIGURE 72

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83551
><subunit 1 of 1, 325 aa, 1 stop
><MW: 37011, pI: 5.09, NX(S/T): 4
MAWSLGSWLGGCLLVSA LGMVPPPENVRMNSVNFKNILQWESPAFAKGNLTFTAQYLSYRIF
QDKCMNTTLTECDFSSLSKYGDHTLRVRAEFADHS DWVNITFCPVDDTIIGPPGMQVEVLA
DSLHMRFLAPKIENEYETWTMKNVNSWTYNVQYWKNGTDEKFQITPQYDFEVLRLNLEPWT
YCVQVRGFLPDRNKAGEWSEPVCEQTHDETVP SWMVAVILMASVFMVCLALLGCFSLLWCV
YKTKYA FSPRNSLPQHLKEFLGHPHNTLLFFSFPLSDENDVFDKLSVIAEDSES GKQNP
G
DSCSLGTPPGQGPQS

Important features of the protein:**Signal peptide:**

amino acids 1-19

Transmembrane domain:

amino acids 222-245

N-glycosylation sites.

amino acids 49-53, 68-72, 102-106, 161-165

N-myristoylation sites.

amino acids 6-12, 316-322

FIGURE 73

CGAGCGCCAAACCGCTAGCGCCTGAATCCGGCGTGCTGCCCGCTCGCCGCCCGCC**ATGG**CCC
 GCGCAGCCCCGCTGCTCGCCGCGTTGACCGCGCTCCTCGCCGCCCGCGCTGCTGGCGGAGAT
 GCCCCGCCGGGCAAAATCGCGGTGGTTGGGGCTGGGATTGGGGGCTCTGCTGTGGCCCATTT
 TCTCCAGCAGCACTTTGGACCTCGGGTGCGAGATCGACGTGTACGAGAAGGGAACCGTGGGTG
 GCCGCTTGGCCACCATCTCAGTCAACAAGCAGCACTATGAGAGCGGGGCTGCCCTCCCTCCAC
 TCCCTGAGCCTGCACATGCAGGACTTCGTCAAGCTGCTGGGGCTGAGGCACCGGCGCGAGGT
 GGTGGGCAGGAGCGCCATCTTCGGCGGGGAGCACTTCATGCTGGAGGAGACTGACTGGTACC
 TGCTGAACCTCTTCCGCCCTCTGGTGGCACTATGGCATCAGCTTCCTGAGGCTGCAGATGTGG
 GTGGAGGAGGT CATGGAGAAGTTCATGAGGATCTATAAGTACCAGGCCACGGCTATGCCTT
 CTCGGGTGTGGAGGAGCTGCTCTACTCACTGGGGGAGTCCACCTTTGTTAACATGACCCAGC
 ACTCTGTGGCTGAGTCCCTGCTGCAGGTGGGCGTCACGCAGCGCTTATTGATGATGTCGTT
 TCTGCTGTCTGCGGGCCAGCTATGGCCAGTCAGCAGCGATGCCCGCCTTTGCAGGAGCCAT
 GTCACTAGCCGGGGCCCAAGGCAGCCTGTGGTCTGTGGAAGGAGGCAATAAGCTGGTTTGT
 CCGGTTTGCTGAAGCTCACCAAGGCCAATGTGATCCATGCCACAGTCACTCTGTGACCCTG
 CACAGCACAGAGGGGAAAGCCCTGTACCAGGTGGCGTATGAGAATGAGGTAGGCAACAGCTC
 TGACTTCTATGACATCGTGGTCACTCGCCACCCCCCTGCACCTGGACAACAGCAGCAGCAACT
 TAACCTTTCAGGCTTCCACCGCCCATTTGATGACGTGCAGGGCTCTTTCAGCCCCACCGTC
 GTCTCCTTGGTCCACGGCTACCTCAACTCGTCCCTACTTCGGTTTCCAGACCCCTAAGCTTTT
 CCCCTTTGCCAACATCCTTACCACAGATTTCCCCAGCTTCTTCTGCACTCTGGACAACATCT
 GCCCTGTCAACATCTCTGCCAGCTTCCGGCGAAAGCAGCCCCAGGAGGCAGCTGTTTGGCGA
 GTCCAGTCCCCCAAGCCCTCTTTTCGGACCCAGCTAAAGACCTGTTCGGTTCCCTATTACTC
 AGTGCAGACAGCTGAGTGGCAGGCCCATCCCCCTATGGCTCCCGCCCCACGCTCCCGAGGT
 TTGCACTCCATGACCAGCTCTTCTACCTCAATGCCCTGGAGTGGGCGGCCAGCTCCGTGGAG
 GTGATGGCCGTGGCTGCCAAGAATGTGGCCTTGCTGGCTTACAACCGCTGGTACCAGGACCT
 AGACAAGATTGATCAAAAAGATTTGATGCACAAGGTCAAGACTGAAGTGTGAGGGCTCTAGG
 GAGAGCCTGGGAACCTTCATCCCCCACTGAAGATGGATCATCCACAGCAGCCAGGACTGA
 ATAAGCCATGCTCGCCCACCAGGCTCTTTCTGACCCCTCATGTATCAAGCATCTCCAGGTG
 ACCTACTGTCTGCCTATATTAAGGGTCCACACGGCGGCTGCTGCTTTTTTTTAAAGGGGAA
 GTAAGAAAAGAGAAGGAAATCCAAGCCAGTATATTTGTTTTATTATTTTTTTTAAAGAAGAA
 AAAAGTTCATCTTCACAAGGTGCTTCAGACTTGGTTTCTTAGCTAGAAACCAGAAGACTACG
 GGAGGGAATATAAGGCAGAGAACTATGAGTCTTATTTTATTACTGTTTTTCTACTACCTACTC
 CCACAATGGACAATCAATTGAGGCAACCTACAAGAAAACATTTACAAACAGATGGTTACAAA
 TAAAGTAGAAGGGAAGATCAGAAAACCTAAGAAATGATCATAGCTCCTGGTTACTGTGGACT
 TGATGGATTTGAAGTACCTAGTTCAGAACTCCCTAGTCACCATCTCCAAGCCTGTCAACATC
 ACTGCATATTGGAGGAGATGACTGTGGTAGGACCCAAGGAAGAGATGTGTGCCTGAATAGTC
 GTCACCATATCTCCAAGCTTCCTGGCAACCAAGTGGGAAAAGAAACATGCGAGGCTGTAGGAA
 GAGGGAAGCTCTTCCTTGGCACCTAGAGGAATTAGCCATTCTCTTCTTATGCAAGATTGA
 GGAATGCAACAATATAAAGAAGAGAAGTCCCCAGATGGTAGAGAGCAGTCATATCTTACCCC
 TAGATGTTTCATCCAGCAGAGAAGAAAGAAAGGTGTTGGGGTAGGATCTTCAGAGGTTAGC
 CTGGTACTTTCTCATCAGACACTAGCTTGAAGTAAGAGGAGAATTATGCTTTTCTTTGCTTT
 TTCTACAAACCCTTAAAAATCACTTGTTTTTAAAAAGAAAGTAAAGGCCCTTTTCATTCAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

75/75

FIGURE 74

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA116510
><subunit 1 of 1, 494 aa, 1 stop
><MW: 54646, pI: 7.27, NX(S/T): 6
MARAAPLLAALTALLAAAAAGGDAPPGKIAVVGAGIGGSAVAHFLQQHFGPRVQIDVYEKGT
VGGRLATISVNBKQHYESGAASFHSLSLHMQDFVKLLGLRHRREVVGSAIFGGEHFMLEETD
WYLLNLFRLWWHYGISFLRLQMWVEEVMEKFMRIYKYQAHGYAFSGVEELLYSLGESTFVNM
TQHSVAESLLQVGVTVQRFIDDVVSAVLRASYGQSAAMPAFAGAMSLAGAQGSLWSVEGGNKL
VCSGLLKLTKANVIHATVTSVTLHSTEGKALYQVAYENEVGNSSDFYDIVVIATPLHLDNSS
SNLTFAGFHPPIDDVQGSFQPTVVSLVHGYNSSYFGFPDKLPFPANILTTDFPSFFCTLD
NICPVNISASFRRKQPQEAAVWRVQSPKPLFRTQLKTLFRSYYSVQTAEWQAHPYGSRPTEL
PRFALHDQLFYLNLEWAASSVEVMAVAANKVALLAYNRWYQDLQDKIDQKDLMHKVKTEL

Important features of the protein:**Signal peptide:**

amino acids 1-19

N-glycosylation sites.

amino acids 185-189, 290-294, 308-312, 312-316, 342-346, 378-382

N-myristoylation sites.amino acids 33-39, 35-41, 38-44, 61-67, 64-70, 218-224, 234-240,
237-243, 429-435